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JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF
SERICULTURAL AND ENTOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE
FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
OS Plautia stali intestine virus
PN WO 02061080-A/1
PD 08-AUG-2002
PP 31-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 JP 01F 016746
PR 25-JAN-2001 JP 018746
PR 0201JF000641
PC C12N15/11,C12N15/86,C12P21/02
CC Novel tertiary structure having ability to accelerate CC translation activity
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BD173511.1 GI:28414842
WO 02061080-A/1.
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Plautia stali intestine virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
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Novel tertiary structure having ability to accelerate
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1 (bases 1 to 188)
Nakashima,N. and Kanamori,Y.
Novel tertiary structure having ability to
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19.7 78000
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19.5 317783
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/organism='Plautia stali intestine virus'.
Location/Qualifiers
                                                               /organism="Plautia stali intestine virus"
/mol type="genomic RNA"
/db_xref="taxon:64698"
   100.0%; Score 188; DB 66.5%; Pred. No. 2e-34;
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7 AF03679088

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AC012404 Human Chr
ACC157128 Bos tauru
AC005510 Homo sapi
AC0142224 Medicago
BX276112 Zebrafish
CR75994 Danio rer
AL929314 Zebrafish
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BX571670 Zebrafish
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AP0036700 Caenorhab
AC156589 Glomus sapi
AL920368 Homo sapi
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AL929357 Plasmodiu
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Novel translational activity-promoting higher-order structure have translational activity-promoting higher-order structure patent: JP 2002306168-A 1 22-CCT-2002;

AL Patent: JP 2002306168-A 1 22-CCT-2002;

PATENTONOLOGICAL HIROSHIMA PREFECTUAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES

OS Plautia stali intestine virus
PN JP 2002306168-A/1
PD 22-CCT-2002
PF 25-JAN-2001 JP 2001016746
PF 25-JAN-2001 JP 2001016746
PF NOBUHIKO NAKASHIMA, YASUSHI KANAMORI NOVEL TRANS/09, C12N1/19, C12N1/19, C12N1/21, C12N5/00, C12R1:92) CC

(C12N15/09, C12R1:92), C12N15/00, (C12N15/00, C12R1:92) CC

NOVEL translational activity-promoting higher-order structure FH Key Environ
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JP 2002306168-A/1.
Plautia stali intestine virus
Plautia stali intestine virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
1. (bases 1 to 188)
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/mol_type="genomic RNA"
/db_xref="taxon:64698"
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                                      AB006531 8797 bp RNA linear Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds AB006531
 Plautia stali
                          AB006531.1
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Nobuhiko,N. and Jun,S.

Nobuhiko,N., and Jun,S.

DNA promoting translational activity into protein and method for efficiently synthesizing protein from protein gene with the use of
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NATL INST OF SERICULTURAL & ENTOMOLOGICAL SCIENCE
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C12N15/09,C12N5/10,C12N7/00,C12P21/02//(C12N15/09,C12R1:92),
(C12N5/10,C12R1:91),(C12N7/00,C12R1:92),(C12P21/02,C12R1:91),
C12N15/00,
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JP 199290084-A/1
26-OCT-1999
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Key Location/Qualifiers
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/db_xref="taxon:32644"
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                           GI:2344756
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 188; DB 6; 66.5%; Pred. No. 1.7e-34; ive 63; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki, J., Nakashima, N., Saito, H. and Noda, H. An insect picorna-like virus, Plautia stali intestine virus, has genes of capsid proteins in the 3' part of the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plautia stali intestine virus Viruses; ssRNA positive-strand viruses, Dicistroviridae; Cripavirus.
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Virology 244 (1),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQVMKAKEESHLTI BPSINNLLATQGWLSWFVDSYEERNDLGYDNFPDEVUTPDQYIE
KFETANIDITPDPKPDEISADKERTTMLWRTHFSQICEEPUTPTQYIE
KFETANIDITPDPKPDEISADKERTTMLWRTHFSQICEEPUT VTALGV
GYTIYRCFFNGETTPLAKSEIVLPKFPESQEKEGVIS GCKEISQEKIGSVSRVRVESQ
EKLGALPHYKLEQSVFNATEDSVNMQCNGNVENLALQNYYSKVNEMLTVEGCSDQNAA
EILSKUVCRNYYALFVCRPDGRESRICGHILFLKDKIGYNPQHFLFSLRKEMEESPDSF
ISLRSIFLRNMYEIYICDFLNYNIFVENDGGRLUVGCLVDVETVTKHPDILTTIVVS
QTEVKSLLRSDVCLPFHHVPESIKYKFYATIAYGTGQSQLVKGGSISSISTYDATFYF
RQSNKYKLQTASGTCGAPVILIGAKQGPGRICGMHVMGDSQGNGYAVALTRELLCKWI
NDLNFTIQSSEMEKKMIQNGVFDTLFFPGKFISLGSPISISASKTQLRKSVLYGEI
APVLTKPTMLTPGTLNGEVUNDFRNYRLSLFGRRFILVKMILLNSILDRLVQRIYVESY
GSNYKYESRYFFFTACEGIDSDFTFNSIKRTSAGYPLCSKVKNGKGEIGSGDGFPNF
KTKLALDLRKDVEHIESLAMDGISSVHVFIDTLKDERKALEKAHKTRLFFASPLFYLI
LCRNYLQGGGSGRLIRGKUNULAVGTNFYSDDWTRVAHHLLRNHEHPVAGDFASYDSSG
EKEILRAACEVIVELCEDLSLFQSGROKHRRUWVLLESLLNSHFYSYGKLYYMSKSL
EKEILRAACEVIVELCEDLSLFQSGROKHRRUWVLLESLLNSHFYSGKLYYMSKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIDKFFTYFEESIVCQDGLKDESQFLSLFLLDKLFLNGCPVSMKNAKDFVWFVSQAFR
FSQGTTHIVSYVKDLYVHCEHFFRVKLIGLFSLSYESFVCTWIERIQDTYEKYKKNIL
VLDARLLDKLFLNYKSEMFRFLCTPSAFRYKOGJTIVKYTNLTYNLIDKYPISQRGGYKNI
LRPPVSLLLLGGTGRGKTTVTFPLTTEVATRIYLEBHEGDITDEDIASSIYARNSEQ
EYWDGYTGQLTTVFDDFMQRVDSASNBVLEIFBRLASSIFFYELHMAKNLEDKNITWF
RSSUTLASSNICTABENLOSKYHBLNYVVALLARFDLVVEVEIAFGCTKRARAQDFFKSNI
KFTKVEYILDESDRVSIVRSEISYDEIVKLMCLKYKDNMTTCQSVSANITEMIGNVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDNYISLTDLTKFRLVSHMERVSSKFLFPQRSTVSLCSDGTILVEDPYTYVQHPQTSY
NVVPPQLNLQSSGNILEDFIRKYETELRFMCGQKKLQGINITHKIDKDDLQAVINSVM
ATVSEQWSQVKGKVLKLFLILVKFLTGLLLVSLGLKILKDLSALSVIKTFLFLLFGMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKDSYSYYSIERMIFEDLHNPYLGNVNHVRKRNFIQPIKRWYDMYNPVCVSFDRKVQG
YGVNWPHFLFLHRHDETESQYNTHHLFRSDVDLVVEYERNCVWFDLSARDVETYSFIL
GLPENIQYNCLDQILDDRFTSEDLFHLIENLQFARKLPLVVFDGKWRFQQPHLSLFKF
                   /translation="qekeftqgrdttaqskripgaqagelnngveyqeqivsfsddam
KIDECLISCAPQTMNESRPASDFREHTIVDFLERPRVVATHIWSTADARNTNLVDLEI
PKALLDNMNLNKFDGFSSFSATVEFKLQINSQPFQAGLLIMGALPSKDLIGSRNTDVK
                                                                                                                                                                                                                                                                                                                                                                                                                        PSGHFLTSIINSIFVNIAMCYAFVESQEKGNRSEENIRVFFNDFSIVTYGDDHVIGVP
EKYVEDFNQLTLPKLLKTLGLDYTMEDKDRICDIKSRKLEEVTFIKRSFRYVKELDRW
LAPLDLNSILDCMNMQRSGEDEGLNAQANVSFALKELSLHPEDVMDQWFPLILRACNK
                                                                                                                                                                                                                                    /note="Bither readthrough of terminal codon of the first orf for nonstructural polyprotein or use of internal ribosome binding site. Confirmed N-terminal of capsid protein precursor starts at 6193 by N-terminal analysis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="nonstructural polyprotein"
/protein_id="BBA21898.1"
/db_xref="GI:2344757"
                                                                                                             /product="capsid protein precursor"
/protein_id="BAA22088.1"
/db_xref="GI:2361038"
                                                                                                                                                                                                                                                                                                                                                                                              hgveveflsrhaafqavretdffeees"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Plautia stali intestine
/mol_type="genomic RNA"
/specific_host="Plautia stali"
/AVDKSLYIPHTLFDISKTSEITLSVPYVSPFPQYNLVLEPINWSNFFIKVYSPLVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MMFSLNSLNSRTDFTDDDLMLLDLEKPVTLFDKEIFRQTLADMC"
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Patent: WO 02061080-A 2 08-AUG-2002;
JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENYOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI OS Himetobi P virus
PN WO 02061080-A/2
PD 08-AUG-2002
PF 31-JAN-2001 WO 2001JP000643
PR 25-JJAN-2001 WO 2001JP000643
PR 25-JJAN-2001 JP 01P
PC C12N15''
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WO 02061080-A/2
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ERMVSMFALLKRBSYAETSTGBLFTYLDLTLRLBSLTSDDTGSYLVBGATTKDNFIAC
NLLSRLVQMFAFYRGGLINIKVAEDKGQVVFBLYSAYLSGLTTSSNTYMSYFESVEGYU
AKSLCEFNYFYYNSFKFSAVATNQTVFNVTQFFFNFLAAGRVAVSAKDDFDCGFFLGF
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GVDTGVPMSAFAGNALPLMSSLGGSDADELSFKYLLQQPNYIDSFSYSSTITSPTTIN
STHLCPFFLSKTDIQGHPQPTLLYYLSNFFLYWRGSLKFTFRFVKTNYHSGRLELVFS
PFSQTQSSDFVNRSAYAYKVVMDLREQTEFSVVIPYNVTRNYSYCDMRTTGPPIDATV
TNPNTVIAHASPGMIAINALTPLQLASELLPTSIDCVVEVSGGDDFELQAPINEGWVG
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                                                           activity
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Location/Qualifiers
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/organism='Himetobi P virus'

.187

/organism="Himetobi P virus"
/mol_type="genomic RNA"
/db_xref="taxon:81583"

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CE 1 (bases 1 to 187)

RS Nakashima,N. and Kanamori,Y.

Novel translational activity-promoting higher-order structure patent: JP 2002306168-A 2 22-0CT-2002;

Patent: JP 2002306168-A 2 22-0CT-2002

ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES

OS Himetobi P virus
PJ 2002306168-A/2
PD 22-0CT-2002
PP 25-JAN-2001 JP 2001016746
PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI POSUHIKO NAKASHIMA, YASUSHI KANAMORI CIZNI5/09,CIZNI/15,CIZNI/15,CIZNI/15,CIZNI/15/00,CIZNI5/00,CIZRI:92) CC (CIZNI5/09,CIZNI-92),CIZNI-92),CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/09,CIZNI-92),CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/09,CIZNI-92),CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/09,CIZNI-92),CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZRI-92),CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZRI:92) CC (CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZNIS/00,CIZNIS
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Himetobi P virus
Viruses; ssRNA positive-strand viruses,
Dicistroviridae; Cripavirus.
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JP 2002306168-A/2.
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translational activity-promoting higher-order structure.
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/mol_type="genomic RNA"
/db_xref="taxon:81583"
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3; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sericultural and Entomological Science, Physiology and Behavior; 1-2 Owashi, Tsu Japan (E-mail:nakaji@nises.affrc.go.jp,
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Nakashima, N. and Sasaki, J.
Direct Submission
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Determining the nucleotide sequence and capsid-coding region of himetobi P virus: a member of a novel group of RNA viruses that
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Himetobi P virus genomic RNA,
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GTNVYSYDWTIIANTLLSKSECMIAGDFEGFDSSQLQDILRAASQVLLNVSRDMLGST
EEDLLVMQVLLESLLSSVHLNNNYVYMWLKGLDSGHFLTAIINSIFVLISFNSVWQIA
FGVNVKKAFEFFEVCGIVAYGDDHIVSVPEWATNVFNQYELASLFKQIGLSYTLEDKD
ATVNAPYRSLNEVGYLKRKFLWDEDKRQYLAPLSLETILETPMWVKKCVDVNLQTTTE
                                                                                                                                                          NSVKRSSSPGYPFVFDKEWNSKEKIFGKGPEFDVTNEKAILLRQQVEEIISQAKLGVR
QQHVFIDTLKDERKDIHKAHKTRMFSACPLDYLIACKMYFGGVVSLLQKSRNICGISV
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DCQIALYYMTRVLYDAKVCSRRVRTAYALCRILNHVPEHLIPYINKDLIENFELCVP
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/protein_id="BAA22553.1"
/db_xref="GI:3493358"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Himetobi p virus"
/mol_type="genomic RNA"
/specific_host="Laodelphax striatellus"
/db_xref="taxon:81583"
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                                         2 (bases 1 to 9275)
Nakashima, N. and Noda, H.
Nakashima, N. and Noda, H.
Direct Submission
Submitted (08-JUL-2004) Nobuhiko Nakashima, National Institute of
Submitted (08-JUL-2004) Nobuhiko Nakashima, National Institute of
Agrobiological Sciences; Owashi 1-2, Tsukuba, Ibaraki 305-8634,
Japan (B-mail:nakaji@affrc.go.jp, Tel:81-29-838-6109,
Fax:81-29-838-6028)
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Himetobi P virus
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TRTAELTRAIDRI IALEHVQLDISEQSSVTLRVPXIS PSYSAVILIBGRYRVGVAV
YSELMQVSQPHKLKVNI FGYYDNVTLGYPTLGTI ALSPVANEQVNILMSEARMKLRIS
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ISFTVPAGTTPFKRIRPEINPLSSGLSVDDFNVFARGVLGYRALTFDLVLGSTVVPS
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GHDIRSDYLEDKIEIKDITGISSNISLNTEKSLSCYGESFGNFRDLIKRFGMFKNQSV
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/protein id="BAA32554.1"
/db_xref="01:3493359"
/translation="ANNNNNNNTNSQKVNDTTFSDRENPSVSAGRIDESVEFTQEIT
/translation="ANNNNNNNNNTNSQKVNDTTFSDRENPSVSAGRIDESVEFTQEIT
/translation="Comparison of the protein of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFTNTKI LSGI PI VNYTSSI AGTGLTLTADGGSTPLTMVSSMYA PFRGGFRAKVY IHD
LPAGEMVQGALI DNSQNTNVPQPLALQSLQYELSDKRLYEFSWPYYCPTYLTTYPSGS
LNY ISDLVNPTTYAR I TTI SEYATA YAMAAADD PDCGFYLGA PLSWNWE I ERLAGRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSYGFVTSPLRVDPFDKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        upstream codon, directed by Internal ribosome entry site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENSLKELCLHPQSVWDSHIESFKHCAKLLGSFPLFLDREFARSFVLNENV"
<6473. .9097
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9275 bp RNA linea:
RNA, complete sequence,
                                                                                                                                                                                                                                                                                                                                                                                                         brown
                                                                                                                                                                                                                                                                                                                                                                                                                                              and Noda, H.
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                                                                                                                                                                                                                                                                                                                                                                                                         planthopper, Nilaparvata
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2 ACUAUGUGAUCUUAUUAAAAUUAGGUUAAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUGC 61

Matches Query Match Best Local

74; Conservative Similarity

43;

34,3%;

Score 64.4; DB 13; Pred. No. 2.1e-05; "" wiematches 66;

Length 9275; Indels

ω --

Gaps

ORIGIN

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TIQILVEMKGGFDFBVECFNSTGMMFIHSITAAATGRUTVDSELVSTAGEQANFASTG
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QAFAKIKIGRAASGTQRQDCRVYGSDPTDRLRLVRCWRYVLETEVGDCGAPLIARNV
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NSVKRSSSPGYPFVFDKEMNSKEKIFGKGPBEDVTNEKAILLRQQVEEIISQAKLGVR
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LYMNLEYVMNPNKDLDLLCGENDSWDQYVLSRQLKEMRAIWVGLQAGNVDPILDTVNP
DCQIALYYMTRVLYDAKVCSRRVRRTAYALCRILNHVPEHLMPYINKDLIENFBLCVP
FRRKLVWYLLKRCLLFSDMPLEIRWKDVCYDBRMYEEKIBEVDEQVFNVASQSRSDIE
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GTNVYSYDWTIIANTLLSKS PCMIAGDFEGFDSSQLQDILRASAGVLLAVSRDMLGST
BEDLLVMQVLLESLLSSVHLANNYVYVMLKGLFSGFFLTAIINSIFVLIEFSSVWQIS
FGVNVKKAFEFFEVCGIVAYGDDHIVSVPEWATNVFNQYELASLFKQIGLSYTLEDKD
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                                                                                                                                                                                             AFSNTKILSGIPIVNYTSNISGTGLTLTADGGSTPLTMVSSMYAFFRGGFRAKVYIHD
                                                                                                                                                                                                                                                            QHDIRSDYLEDKIEIKDITGIPSNVSLNTEKSLSCVGESFGNFRDFIKRFGWHKNQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directed by internal ribosome entry site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATVNAPYRSLNEVSYLKRKFLWDEDKRQYLAPLSLETVLETPMWVKKCVDVNLQTTTE
LENSLKELCLHPQSVWDSHIESFKHCAKLLGSFPLFLDREFARSFVLNENV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:81583"
/lab_host="Nilaparvata
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/isolate="Izumo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="translation starts at GCU (alanine) triplet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSQLIQTKISSYKNYVNRKIKEERSNIHPLLRATPNFVEDVESD/
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                JOURNAL REFERENCE
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AC120366
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ORGANISM
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AX786480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 ACCCUCGUGCUCACAACAUUAAGUGGUGUUGUGCGAAAAAGAAUCUCACUU 188
Unpublished
( thases I to 156784)

2 (bases I to 156784)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Barren,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,

Anderson,S., Barwan,A., Camarata,J., Campopiano,A., Chang,J.,

Boukhgalter,B., Brown,A., Colangelo,M., Collins,S., Collymore,A.,

Chazaro,B., Cheepel,Y., Colangelo,M., Collins,S., Collymore,A.,

Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

Faro,S., Ferreira,P., FitzHugh,W., Graham,L., Grand-Pierre,N.,
                                                                                                                                                                                                                                                                                                                                                            AC120366
AC120366.9
HTG.
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                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 156784)
Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                               Mus musculus chromosome 1, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                            AC120366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plautia stali intestine virus
Plautia stali intestine virus
Viruses, ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 from Patent WO03020928
AX786480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Atabekov, J., Dorokhov, Y., Skulachev, M.L., Ivanov, P. and Gleba, Y. Identification of eukaryotic internal ribosome entry site (ires)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX786480.1 GI:32953901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCTCGTGCTCGCTCAAACATTAAGTGGTGTTGTGCGAAAAGAATCTCACTT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACATTITTAAGACCCTTAGTTATTTAGCTTTACCGCCCAGGATGGGGTGCAGCGTTCCT 6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUCACU 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAAUAUCUAGUGUACCCUCGUGCUCGCUCAAACAUUAAGUGGUGUUGUGCGAAAAGAAU 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAATATCCAGGGCACCTAGGTGCAGCCTTGTAGTTTTAGTGGACTTTAGGCTAAAGAAT 6465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UAUAGUCUUAGAGGUCUUGUAUAUUUAUACUUACCACACAAGAUGGACCGGAGCAGCCCU 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO 03020928-A 12 13-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Plautia stali intestine virus"
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/db_xref="taxon:64698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   GI:52138829
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71.7%;
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Pred. No. 0.027;
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Hagge, B., Hortch, L., Halme, W., Iliev, I., Johnson, R., Jones, C., Kamatr, A., Karatasa, K., Kalls, C., Lamcarete, R., Lamca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/MIT Center for Genome Research Center code: WIBR
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                                                                                                           /rpt_family="Lx4"
10197. 10477
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complement(3. .135)
/rpt_family="Lx2"
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/db_xref="taxon:10090"
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_family="Charlie4"
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                                           Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F. Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'S.
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus. 1 (bases 1 to 155949)
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| 11906_ .11963
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/rpt_family="MTD"
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17139. .17348
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15883. .1625'
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complement(15022. ...
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/rpt_family="RMER12"
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complement(11967 .12)
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16256. .16421
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Eggn. A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Eggn. A., Escotto, M., Elgene, C., Evans, C.A., Falls, T., Fan, G., France, C.A., Falls, T., Fan, G., Fan, G., Falls, T., Fan, G., Fan, G., Falls, T., Fan, G., Falls, T., Fan, G., Falls, T., Fan, G., Falls, T., Fan, G., Fan, G., Falls, T., Fan, G., Falls, F., Falls, 
                                                                                                                                                                                                                                                                                                                                          AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23915360.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecte/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                  Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109093 TAAAAATGAGGTTTAATATTGCTAAAGACAGAGAGGTCATGGCGATTTTCACGGAGCATG 109152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109153 CÁGCATGCAGGGGÁGCCGGGCTC 109175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 CAAGAUGGACCGGAGCAGCCCUC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 UUAAAAAUAGUUUUAAUAUUGCUAUAGUCUUAGAGGUCUUGUAUAUUUUAUACUUACCACA 99
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 243160)

Muzny D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
                                                                                                                                                                                                                                                                                               243160 bp
Rattus norvegicus clone CH230-15D5,
unordered pieces.
ACOBRACA
                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                               AC098490.5
                                                                                                                                                                                                                                                                                         AC098490
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 153428 bases at least Q40 Consensus quality: 154322 bases at least Q30 Consensus quality: 154724 bases at least Q20 Estimated insert size: 156661; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: CH230-448E18
------ Summary Statistics
Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: KAKS
Center clone name: CH230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CH230-448E18"
complement(1736. .2514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (148932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 152687: contig of 152687 bp in length
8 152787: gap of unknown length
8 155949: contig of 3162 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                estimated_length=unknown/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .. .155949
                                                                                                                                                                                                                                                            GI:30521857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence:BZ251602"
88. .152787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _sequence:BZ251604"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 39.8; I
49.4%; Pred. No. 8.6;
ive 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                DNA
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                                                                                                                                                                                                                                                                                                                                   linear HTG 10-
G DRAFT SEQUENCE,
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Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blakr, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, M., Bhaky, C., Burch, P., Burrell, K., Calderon, E., Bryant, M., Bhaky, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chave, J., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chave, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Devis, C., Davy, Carroll, L., De Anda, H., Davis, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, R., Chen, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugena, C., Evans, C.A., Falls, T., Fean, G., Ferrandez, S., Finley, M., Flagy, M., Garcia, A., Garner, T., Garza, M., Gunrartne, P., Haeland, W., Hamilt, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, U., Herrandez, J., Haeland, W., Hanil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, U., Herrandez, J., Liu, J., Liu, W., Liu, Y., London, P., Londson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kel
submitted (10.MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:23101361.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 243160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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REFERENCE AUTHORS

JOURNAL

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COMMENT

JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

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RESULT 13
AC146773
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                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 CAAGAUGGACCGGAGCAGCCCUC 122
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                                                                                                                                                                                                                                                                                         174327 bp DNA linear HTG 01-OCT-2003
Didelphis virginiana clone LB3-175022, WORKING DRAFT SEQUENCE, 5
Ordered pieces.
                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT.
Didelphis virginiana (North American opossum)
                                                                                    Didelphis virginiana
                                                                                                                                                                                                                  AC146773.1 GI:37202147
                                                                                                                                                                                                                                                                   AC146773
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 21.2%; Score 39.8; D
Similarity 49.4%; Pred. No. 7.9;
41; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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235050
236264
236364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
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234950 .235049
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-15D5"
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clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.hgsc.bcm.tmc.edu/
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ORIGIN
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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                                                                                                      gap
                                                    gap
                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 103877: contig of 103877 bp in length
103978 103977: gap of unknown length
110557 119382: contig of 6679 bp in length
110557 139382: contig of 28626 bp in length
1139483 139482: gap of unknown length
1139483 139482: gap of unknown length
1148218 148317: gap of unknown length
1148218 174327: contig of 8735 bp in length
1148318 174327: contig of 26010 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the description: http://www-gsd.lbl.gov/cheng/BAC.html These libraries are available through the BACPAC Resources Center: http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: O140
Bac Clone Name: LB3-175022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-OCT-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 174327)
2 (bases 1 to 174327)
Cheng, J.-F., Hamilton, M., Peng, Y.,
Peng, Z., Malinov, I. and Rubin, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avid (http://baboon.math.berkeley.edu/mavid),
Lagan (http://lagan.stanford.edu/) and paired end information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=RUNX1
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Direct Submission
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Cheng, J.-F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Funding agent: Programs for Genomic Applications (NHLBI)
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                                                                                                                                                                            Bource
                                                                                                                                                                                                                                                                      regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: RMBL; Sw., SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by The Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 6, 2003 this sequence version replaced gi:28172267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
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Actinopterygil; Neopterygil; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 159758)
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Zebrafish DNA sequence from clone CH211-160M22, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                         organism="Danio rerio"
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Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 34.6 | 34.8 | 35 | 35 | 35.8 | 35.8 | 36.2 | 36.2 | 37.2 | 39 | 53 | 64.4 | 64.4 | 68 | 181.6 | 188 | 188 | 188 | 188 | Score |
| 18.4 | 18.5 | 18.6 | 18.6 | 19.0 | 19.0 | 19.3 | 19.3 | 19.8 | 20.7 | 28.2 | 34.3 | 34.3 | 36.2 | 96.6 | 100.0 | 100.0 | 100.0 | 100.0 | Query |
| 188 | 8392 | 2000 | 2000 | 144460 | 1099 | 11422 | 11422 | 9829 | 39 | 56 | 199 | 187 | | 281 | 430 | 200 | 197 | 188 | Query Match Length DB |
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| ABZ80710 | ABL33491 | ADA68846 | ABZ17361 | AAZ93815 | ADC86196 | ABL32219 | ABK39937 | AAL60324 | AAL50554 | ACC48199 | AAL50545 | ABZ80708 | AAL50552 | AAL50551 | AAZ35832 | AAL50544 | AAL50556 | ABZ80707 | ID |
| Abz80710 Cricket p | Abl33491 Human imm | Ada68846 Arabidops | Abz17361 Arabidops | Aaz93815 Olfactory | Adc86196 Human GPC | Abl32219 Human imm | Abk39937 Human che | Aal60324 Aphid let | Aal50554 CrPV-like | Acc48199 Insect vi | Aal50545 Himetobi | Abz80708 Himetobi | Aal50552 CrPV-like | Aals0551 CrPV-like | Aaz35832 Plautia s | Aal50544 Plautia s | Aal50556 CrPV-like | Abz80707 Plautia s | Description |

The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

range of

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

WPI; 2003-403230/38.

Nakashima N,

Shibuya N,

Nishikawa

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Claim 1; Page 31-32; 39pp; Japanese.

| | | a | ^ | | | | | a | | a | o | | | | | | | n | | | o | | | | |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|
| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | | 36 | 35 | | IJ U | 32 | 31 | 30 | 29 | 28 | | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
| ມ | 33 | 33.2 | 33.2 | 33.2 | 33.2 | 33.2 | 33.2 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.8 | 34.2 | 34.2 | 34.2 | 34.4 | 34.4 | 34.6 | 34.6 |
| 17.6 | 17.6 | 17.7 | 17.7 | 17.7 | 17.7 | 17.7 | 17.7 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 18.0 | 18.2 | 18.2 | 18.2 | 18.3 | 18.3 | 18.4 | 18.4 |
| 2000 | 2000 | 77522 | 32359 | 2442 | 1378 | 1366 | 500 | 245531 | 110000 | 110000 | 54945 | 7040 | 7040 | 7040 | 7040 | 7040 | 7040 | 63609 | 6227 | 6227 | 541 | 10480 | 5586 | 18011 | 200 |
| Ð | δ | 13 | H | 4 | 12 | 12 | 14 | 13 | 10 | 10 | œ | 10 | 8 | œ | œ | δ | 4. | 12 | σ | σ | 12 | თ | σ | σ | 9 |
| ABZ15854 | ABZ16012 | ADS36495 | ACN44720 | AAI69728 | AD077805 | AD077806 | ADZ70941 | ABD33022 | ACF65386_2 | ACF67367_26 | ACC70517 | ADE84115 | ADA84155 | ADA20348 | ABZ10033 | ABK33963 | AAS46439 | ADQ97537 | ABL92260 | ABL33586 | ACH71783 | ABL34201 | AAS63357 | ABL32035 | AAL50547 |
| Abz15854 Arabidops | Abz16012 Arabidops | Ads36495 Human aut | Acn44720 Mouse gen | Aai69728 Microtubu | Ado77805 Pea legum | Ado77806 Experimen | Adz70941 Human chr | Abd33022 Human can | Continuation (3 of | Continuation (27 o | Acc70517 Human sph | Ade84115 Human lym | Ada84155 Human ren | Ada20348 Prostate | Abz10033 Haematopo | Abk33963 Human DNA | Aas46439 Tumour su | Adq97537 Human can | Ab192260 Chemicall | Abl33586 Human imm | Ach71783 Human gen | Abl34201 Human imm | Aas63357 Chemicall | | Aal50547 Cricket p |

ALIGNMENTS

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RESULT 1
ABZEGOT 1
ABZEGOT 15-C
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ABZEG ABZEG XX
ABZEG ABZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ80707 standard; RNA; 188 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001; 2001JP-00319923.
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RESULT 2
AALSO556
ID AALS
AC AALS
AC AALS
AC AALS
AC CrPV
KW CrPV
KW CrPV
KW drug
KW prot
OS Unid
XX Unid
FT misc
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Matches 188
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                                                                                                                                                                                                                                                                                                                                                                                                         CrPV-like virus; ss; higher-order structure; drug drug production; translational activity-promoting
                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                 protein synthesis; structural analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CrPV-like virus-related RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL50556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the plantia stall intestine virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing useful proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 188 BP; 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; RNA; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCUCACUU 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UCCAAUAUCUAGUGUACCCUCGÜĞCUCGCÜCAAACAUUAAGUGGÜGÜÜGÜĞÇĞAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UCCAAUAUCUAGUGUACCCUCGUGCUCGCCUCAAACAUUAAGUGGUGUUUGUGCGAAAAGAA 180
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function;
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                                                                                                                                           d RNA
with
                                                                              sequence #6"
bases 110-107
                                                                                                                                          sequence |
bases 7-1
                                                                                                                                                                                                       sequence #6"
bases 142-138
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bases 68-
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Query Match
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                                                                                                                           The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in tsynthesis of proteins and polypeptides for application in developing a producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gent recombinant technique. The present nucleotide represents an RNA sequences that was used in an example of the invention
                                                                                                                                                                                                                                                                           Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                       Sequence 197
                                                                                                                                                                                                                                            Example 1; Fig 6; 38pp; Japanese
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184. 188
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a double-stranded region with
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                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CrPV-like virus-related RNA sequence #6" double-stranded region with bases 188-184
                                                                 188;
No. '
                                                             4.2e-43;
                                                                          Length 197;
                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence #6"
bases 163-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence #6"
bases 149-146
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bases 174-171
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bases 39-35
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Matches 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                   Sequence 200 BP; 66 A; 34 C; 37 G; 0 T; 63 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1-2; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001; 2001JP-00016746.
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                                                                                                                                                                                                                                                                                                                                                                                                        intestine virus RNA sequence of the invention
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                                                                                                                                                                                                                                                       188;
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  UCCAAUAUCUAGUGUACCCUCGUGCUCGCUCAAACAUUAAGUGGUGUUGUGCGAAAAGAA 180
                                                                            CUAUAGUCUUAGAGGUCUUGUAUAUUUJAUACUUACCACACACAAGAUGGACCGGAGCAGCCC 120
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                                                                                                                                                                                                                                                  100.0%; Score 188; DB 6; 100.0%; Pred. No. 4.2e-43; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a Plautia stali intestine virus (PSIV) CC translation promoting sequence. Also described in the present invention CC are: (a) a plasmid having a gene for synthesising the objective protein CC downstream of the above DNA base sequence; (b) a plasmid in which the CC above DNA base sequence is inserted between the promoter sequence and the CC translation starting point of the objective gene; (c) a transformant in CC which the above plasmid is introduced to a host cell, a recombinant CC baculovirus having a gene for synthesising the objective protein CC in which the above DNA base sequence; (d) a recombinant baculovirus cell infected by the above recombinant baculovirus of the objective gene; (e) a cultured cell infected by the above recombinant baculovirus; and (f) a method for synthesizing efficiently a protein from a protein gene compositioned downstream by taking a DNA corresponding to a base sequence CC promoting translation activity in the gene base sequence of an insect RNA curus into a plasmid. The translation activating DNA is used for synthesising the encoded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA promoting translation activity to a protein - and synthesis protein efficiently from a protein gene by using the DNA.
                                                                                                                                                                                                                                                                                                                                                      Sequence 430 BP; 131 A; 80 C; 93 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-016983/02
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                                                                                                                                                                                                                                                    100.0%; Score 188; DB 3; 66.5%; Pred. No. 4.9e-43; tive 63; Mismatches 0
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  Query Match
                                                                                                              The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents an RNA sequence
                                                                                                                                                                                                                                                                                                                                                                      Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                              Sequence
                                                                                                                                                                                                                                                                                                         Example 1; Fig 3; 38pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakashima N,
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translational activity-promoting function;
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                                                                                                                                    Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function; protein synthesis; structural analysis.
                                                                  Example 1; Fig 5; 38pp; Japanese.
                                                                                                                                                                                                                                            WPI; 2002-627482/67.
                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001; 2001JP-00016746.
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                                                                                                                     in drugs.
                                                                                                                                                                                                                                                                                             Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CrPV-like virus-related RNA
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62. .68
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "CrPV-like virus-related RNA sequence #2"
/note=""Forms a double-stranded region with bases 68-62
of itself"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /bound_moiety= "CrPV-like virus-related RNA sequence note= "Forms a double-stranded region with bases 7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.8e-41;
                                                                                                                                                                                                                                                                                                                                             SCI.
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The invention comprises seven RNA a have a higher-order structure that

sequences sustains

(CrPV-like viruses) translational activi

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RESULT 7
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ពួកក្រកួត
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Best Local S
Matches 68
                                                                               The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the himetoble p virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABZ80708 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents an RNA sequence that was used in an example of the invention
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 32; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudoknot; secondary structure; cell-free protein synthesis; albumen; impurity; higher-order structure; intergenic region; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Himetobi P virus derived pseudoknot sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002; 2002WO-JP010447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibuya N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
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Pred. No. 1.8e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wheatgerm;
IGR-IRES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Query Match

Sequence 187

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Query Match Best Local :

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Score 64.4; DI Pred. No. 2.3e 0; Mismatches

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                       The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Himetobi P virus RNA sequence of the invention
                                                                                                                                                                                                    Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CrPV-like virus; ss; higher-order structure; drug drug production; translational activity-promoting protein synthesis; structural analysis.
Sequence 199
                                                                                                                                                            Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                 WPI; 2002-627482/67.
                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2001; 2001WO-JP000641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Himetobi P virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Himetobi P virus RNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL50545;
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BP; 60 A; 33 C; 40 G; 0 T;
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); Mismatches
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66 U; 0 Other;
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                                                                  Query Match
Best Local S
Matches 53
                                                                                                                                                     (IRES) element from the insect RNA virus, Plautia stall intestine virus (PSIV). The invention provides a method of creating an artificial IRES element having an adenine-rich (40-100 mol*) nucleic acid block of at least 25 nucleotides and capable of causing cap-independent translation of a downstream nucleotide sequence of interest in eukaryotic cells, such as plant, animal or yeast cells (claimed). A method of identifying nucleic acid elements having IRES activity involving genome database searches is also provided. The methods allow the creation or identification of IRES elements that are universal with cross-kingdom and
                                                                                                                     Sequence 56
                                                                                                                                                                                                                                                                                                                                     Creating nucleic acid sequence for carrying out translation by ribosome entry site element and expressing nucleotide sequence interest in eukaryotic cell, by creating a nucleic acid having
                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 48pp; English.
                                                                                                                                                                                                                                                                           The present sequence is that of a known internal ribosome entry
                                                                                                                                                                                                                                                                                                                                                                                                                     Atabekov J,
                                                                                                                                                                                                                                                                                                                                                                                                                                               (ICON-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plautia stali intestine virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Internal ribosome entry site; IRES; translation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-2003
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                                          136
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                                                                                                                   BP; 16 A; 14 C; 11 G; 0 T; 15 U; 0 Other;
                                                                                                                                              activity
                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETICS
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                                                                  0;
                                                                              Score 53;
Pred. No.
                                                                  Mismatches
                                                                              DB 8; Le
2.9e-05;
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                                                                  0
                                                                                         Length 56
                                                                  Indels
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RESULT 10
AAL50554
ID AAL50
XX AL50
XX AL50
XX CrPV-
XX CrPV-
XX CrPV-
XX drug
XX drug
XX drug
XX drug
XX drug
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                                                                                                       Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                 The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents an RNA sequence that was used in an example of the invention
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2001; 2001WO-JP000641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 5; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001JP-00016746.
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Н
                                                                                                                                   Similarity
                                                ACACAAGAUGGACCGGAGCAGCCCUCCAAUAUCUAGUGU 135
                                                                                                                                                                                                                 39 BP; 12
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                                                                                                       20.7%; S
llarity 100.0%;
Conservative 0;
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/note= "Forms a
of itself"
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30. .39
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/bound_moiety= "CrPV-like virus-related RNA
/note= "Forms a double-stranded region with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                       k; Score 39; DB
k; Pred. No. 0.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "CrPV-like virus-related RNA sequence #4" double-stranded region with bases 39-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #4
                                                                                                                                DB 6;
                                                                                                                                                          Length 39;
                                                                                                       <u>..</u>
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bases 10-1 o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel RNA derived from an ALPV (Aphid lethal paralysis virus). ALPV RNA is useful for controlling homopterous insects such as aphids or white files. It is useful in the research concerning aphids and for controlling aphids and in the field of agriculture or floriculture. It is also useful for detecting ALPV- viruses using PCR and for preparing a monoclonal antibody against antigen which is synthesised in vitro. The invention is also useful in gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid derived from aphid lethal paralysis virus, useful detecting ALPV-viruses, for preparing a monoclonal antibody against antigen, in research concerning aphids and for controlling aphids.
Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
                            Human chemically pretreated gene sequence #9 strand
                                                              21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9829 BP; 3083 A; 1906 C; 1879 G; 0 T; 2961 U; 0 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is ALPV RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 10-13; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2001; 2001NL-01019225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL60324 standard; RNA;
                                                                                                                           ABK39937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT RES INT
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Der Wilk F,
                                                                                                                                                                                                                                                                                                                                   6635 GAUUAAUUACUAAUUUGAUCUUUAGGUUAUAAUGUUAGGACUAUAAAAAUUAGCUUAAUG 6694
                                                                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        white fly; agriculture; gene therapy; ss
                                                                                                                                                                                                                                                                                                c-uauagucuuagaggucuuguauauuuuauacuuaccacacaagauggaccggagcagcc 119
                                                                                                                                                                                                                                                                                                                                                         GACUAUGUGAUCUUAUUAAAAUUAGGUUAAAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUG 60
                                                                                                                          standard;
                                                                                                                                                                                                                                   cuccaauaucuaguguacccucgugcucgcucaaacauuaaguggu 165
                                                                                                                                                                                                                                                                   CCACGAAAUCUAGAUUAGUCCGAAUGUCCUAUUUUGAUUAGGUGGU
                                                                                                                                                                                                                                                                                                                                                                                               19.8%;
ilarity 55.4%;
Conservative
                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Munster M;
                                                                                                                           DNA;
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                                                                                                                                                                                                                                                                                                                                                                                               Score 37.2; DB Pred. No. 2.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 9829;
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ABL32219; 26-MAR-2002

(first entry)

ABL32219 standard; DNA; 11422 BP

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                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid comprising a sequence at least 18 CC bases in length of a segment of the chemically pretreated DNA of genes CC associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM 000693), CYP11A (NM 000781), CYP1B1 (NM 00097), CYP3A3 (C (NM 000776 and NM 017460), DPYD (NM 00010), EPHX2 (NM 001979), OCIN (NM 002538), TXNRDI (NM 00330), UGT8 (NM 003360), TMRP (NM 004996, CC NM 019900, NM 019901, NM 019902, NM 019862, NM 019898, NM 019899) and CC their complementary sequences, or a sequence (S1) chosen from 87 CC sequences and their complements. The chemical pretreatment is bisulphite creatment to convert cytosines (but not methyl-cytosines) into uracils. CC later included are an oligomer (II) in particular an oligomucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is dentical to a chemically pretreated DNA of genes associated with CC pharmacogenomics and their complements, arranged in an array for cetecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The colligomers may also be used as DCR primers. The set of 87 nucleic acids and their complements associated with the methylation state (CpG) and/or CC detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The sequences or its complements suseful for diagnosis and therapy of solid cumours and cancer. The present sequence represents one the 87 DNA CC sequences or its complement. Note: The sequence data for this patent did cc tentronic format directly from MIPO at the sequence data for this patent did cc electronic format directly from WIPO.
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
                                                                                                                                                                                                                                                              Sequence 11422 BP; 3913 A; 59 C; 1856 G; 5594 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2001; 2001WO-EP007470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; T:
UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-2002
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                                                                                                                                                                                         Local
                                       73
                                                                                                                 13 UUAUJAAAJUUAGGUUAAAJUUUCGAGGUUAAAAAJUAGUUUUJAAUAUUGCUAUAGUCUUAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPIGENOMICS AG
                                                                                                                                                                                               Similarity
                                                                                   Piepenbrock C,
                                       AGGUCUUGUAUAUUUUAUACUU 93
                                                                                                                                                                             Conservative
                                                                                                                                                                                             19.3%; Score 36.2; DI 28.4%; Pred. No. 4.4;
                                                                                                                                                                        30;
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                             28;
                                                                                                                                                                                                                    Length 11422;
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ARESULT 14
ADC86196/c
ID ADC861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, caucer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HTV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01ek
               Homo sapiens
                                                   ds; gene; human; GPCR;
guanosine triphosphate-binding protein coupled receptor; gene therapy.
                                                                                                                       Human GPCR gene SEQ ID NO:649
                                                                                                                                                                  01-JAN-2004
                                                                                                                                                                                                                                                     ADC86196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 192; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-130909/17.
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 23; Conserv
                                                                                                                                                                                                                                                                                                                                                               2641
                                                                                                                                                                                                                                                                                                                                                                                                                                          2581 TGATTTAAAGTTTTTTGTTATTTGATATTAATATTTTTAGATATTAAAGTTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPIGENOMICS AG.
                                                                                                                                                                                                                                                     standard; DNA; 1099
                                                                                                                                                                                                                                                                                                                                                                                      AGGUCUUGUAUAUUUUAUACUU 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11422 BP;
                                                                                                                                                                                                                                                                                                                                                               AGGTATTTTATTGTTTTAGTT 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UUAUUAAAAUUUAGGUUAAAUUUCGAGGUUAAAAAUAGUUUUUAAUAUUGCUAUAGUCUUAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000DE-01032529
2000DE-01043826
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3913 A; 59 C; 1856 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment of chemically modified gene, of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.2; DB 6;
Pred. No. 4.4;
0; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5594 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ease; AIDS; epilepsy;
psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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           AAZ93815/c
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AC AAZ938:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                          Olfactory receptor protein; olfactory; smell; receptor; binding; detection; screening; genotyping; biallelic marker; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                            Olfactory receptor operon.
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                                                          allele
                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                 AAZ93815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847
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)B; ADC86197.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 AAUUAGGUUAAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUGCUAUAGUCUUAGAGGUCUU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTGATTTTACTTCAAAAGCACGTTTCTTCTGATCAGTTTCCAAAAAAGCTTGTTTCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                      entry)
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"Polymorphic base
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Pred. No. 3
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82; 10;

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Gaps

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Length 1099; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding ten different olfactory receptor proteins and their biallelic markers, are useful in genetic analysis and in screening for compounds which bind to the receptor proteins.
                                                                                                                                                                                                                                             Sequence 144460 BP; 46068 A; 27088 C; 26615 G; 44676 T; 0 U; 13 Other;
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                             140 UCGUGCUCGAAACAUUAAGUGGUGUUGUGCGAAAAGAAUCUCAC 186
                                                                                                                                                    See GENESEQ records AAZ93816-25 and AAY83386-95
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TCCTTGTTCCTCAAACTATAGATGATGGGGTTCAACATAGGGCTTAC
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ALIGNMENTS

| Query Match Best Local Matches 4 | ORIGIN | FEATURES SOUTCE | TITLE JOURNAL COMMENT | ACCESSION VERSION KEYWORDS SOURCE ORGANISM | RESULT 1 CL403205 LOCUS DEFINITION |
|--|---|--|---|--|--|
| Query Match 20.4%; Score 38.4; DB 10; Length 381; Best Local Similarity 39.2%; Pred. No. 10; Matches 47; Conservative 22; Mismatches 51; Indels 0; Gaps 0; | /Organism="Zea mays" /mol_type="genomic DNA" /cultivar="B73" /db xref="taxon:4577" /clone="ZwMBBb0412F06" /lab host="E. coli DH10B" /clone 1lb="ZwMBBb (HindIII)" /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII" | Wersity Wersity Frelinghuysen Road, Piscataway, NJ 08854, USA: 732 445 3801 1732 445 5735 11: bharti@waksman.rutgers.edu primer: T7 psies: BAC ends se: BAC ends Location/Qualifiers 1381 1381 Coration="Zea mays" | hharti, N.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c) Unpublished (2003) Contact: Bharti,A.K. Dr.Joachim Messing's lab Dr.Joachim Messing's lab | CL403205.1 GI:45213390 GSS. Zea mays Zea mays Zea mays Sea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea. | CL403205 381 bp DNA linear GSS 05-MAR-2004 ZMMBBb0412F06f ZMMBBb (HindIII) Zea mays genomic clone ZMMBBb0412F06 5', genomic survey sequence. |
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CG155911.1 GI:
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               Zea mays
Zea mays
                                           CG050490.1
GSS.
                                                                                                                                                                                                                                                                                      l Similarity 47; Conser
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Zea mays
                                                                   genomic survey sequence
CG050490
                                                                                              PUJCX20TD ZM_0.6_1.0_KB
                                                                                                            CG050490
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUIMJ87TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
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PUIMJ87TD ZM_0.6_1.0_KB Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clade; Panicoideae; Andropogoneae;
1 (bases 1 to 715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 301-838-0208
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AAATTAGGTGGTATAACGAGGGGAAAATTATATTTTACATTTTTATCATTTTATGA 212
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                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                    /clone="ZMMBTa0616006"
/clone=lib="ZMC0,610,0 KB"
/note="Vector: pCR4-TOPO; Site 1:
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="B73"
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                                                        GI:33922670
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Pred. No. 10;
22; Mismatches
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                                                                                             DNA linear GSS 19-AUG-2003 genomic clone ZMMBTa0639D16,
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117 AAATTAGGTGGTÄTAACGAGGGGAÄÄÄÄTTÄTATTTTÄCÄTTTTÄTCATTTÄTTAATGA 176
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                                                                                                   9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                              Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHOL18TB Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC438918
PUHOL18TD ZM_0.6_1.0_KB
genomic survey sequence.
CC438918
                                                                                                                                                                                                                                                                                             1 (bases 1 to 958)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoldeae; Andropogoneae; Zea.
                                                                                   Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                    Bennetzen, J
                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC438918.1
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1 (bases 1 to 930)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: whitelaw@tigr.org
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Fax: 301-838-0208
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Location/Qualifiers
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/mol_type="genomic D
/strain="B73"
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/clone_lib="ZM_0.6_1.0_KB"
/clone="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
/note="Vector: pCR4-TOPO; Site_1"
COT selected genomic DNA library"
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39.2%; Pred. No. 10;
tive 22; Mismatches
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a; Poales; Poaceae; PACCAD
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CZ951756
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 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263042 Tomato EcoRI BAC Library Lycopersicon esculentum clone SL EcoRI0053E09 5, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                     Email: sgn-feedback@sgn.cornell.edu
Plate: 53 row: E column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornell University
251 Emerson Hall, Ithaca, NY 14853, USA
Tel: 607-255-6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2005)
Other_GSSs: 267643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC end sequencing from three Solanum lycopersicon libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller,L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamilds; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum
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GAUCUUAUUAAAAUUUAGGUUAAAAUUUCGAAGGUUAAAAAUAGUUUUAAAUAUUUGCUAUAGUC 68
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ller,L.A., Buels,R.M., Wang,Y., Tanksley,S.D., Giovannoni,J.J.,
                                                                                                                                                                                                                                                                                                                                   quality sequence start: 4 quality sequence stop: 544.
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/db_xref="taxon:4577"
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/clone_1ib="ZM_0.6_1.0 KB"
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CoT selected genomic DNA library"
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/clone_lb="Tomato EcoRI BAC Library"
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|mol_type="genomic DNA"
|cultivar="Heinz 1706"
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                                                                                    Score 37.8;
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Pred. No. 10;
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                                                                                                     DB 10;
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                                                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 ATGTATTTTAACATTAGAACTACCTAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila The BDGP is constructing a physical map of
                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enqualmery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 84C14.
part of the Daniokey BAC Library created by R. Plasterk ar
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                     Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                CNSODEVL 1101 bp DNA linear GSS 04-UUN-19
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-JAN-2003) The Sanger Institute, Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio
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BX134773
                                                                                                                                                                                                                                                                                               fly), genomic survey sequence. AL069706
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Humphray, S.J., Huck
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-84C14"
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38.0%; Pred. No. 17;
tive 23; Mismatches
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     the Drosophila
                   Genome Project
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                                                                          segref@genoscope.cns.fr
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ence T7 end of BAC:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C. Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 180genic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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CL448388.1 GI:45693617
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                        Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dr. Joachim Messing's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 Frelinghuysen Road, Piscataway, NJ 08854, USA
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                                                                                                                                                                                         quality sequence start: 104.
Location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="B73"
                                                   /organism="Zea mays"
/mol_type="genomic D
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|mol type="genomic DNA"
|/db_xref="taxon:7227"
|/clone="BACR29B23"
|/clone_lib="RPCI-98"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AAATTAGGTGCTTTAACGAGGGGAAAATTATATTTTACATTTTATCATTTTATTAATGA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 UGUAUAUUUAUACUUACCACACAAGAUGGACCGGAGCCACCCCCAAUAUCUAGUGUACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AAAUUAGGUUAAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUGCUAUAGUCUUAGAGGUCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralph, S., Kolosova, N., Oddy, C., Cooper, D., Butterfield, Y., Kalph, S., Kolosova, N., Oddy, C., Cooper, D., Barber, S., Yang, G., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M. F., Rilland, C. E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.

The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries

Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard,
Vancouver, British Columbia, Canada, V6T 1Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bohlmann@msl.ubc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 1-604-822-0282
Fax: 1-604-822-2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
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                                                                                                                                                                                                                                                                                                          /organism="Picea sitchensis"
/mol type="mRNA"
/culTivar="Gb2-229"
/db_xref="taxon:3332"
/clone="WS01026_D16"
/sex="Hermaphrodite"
/clone_lib="SS-R-N-A-11"
/note="Organ: Roots; Vector: pBluescript II SK (+) XR
/note="Organ: Roots; Vector: pBluescript II SK (+) XR
Site_1: EcoRI (5' end of cDNA); Site_2: XhoI (3' end
cDNA); mRNA was isolated from each tIssue source
independently and equal quantities of mRNA from each
tissue were then pooled. cDNA was prepared from 5
micrograms of mRNA and directionally ligated into the
                                                                                                                                                          /tissue_type="Young root growth (terminal 1-3 cm) and old root growth (distal to terminal 1-3 cm) tissues" /dev_stage="three year old clonal trees grown under greenhouse conditions in standard potting soil mixture." /lab_host="E. coli DH10B cells" /clone_lib="SS-R-N-R-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1:
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Z., Samuelson, J., Clark, C.G., Eichinger, D., Dellen, K., Hall, N., Anderson, I. and Loftus, B. Gene discovery in the Entamoeba invadens genome Hochem. Parasitol. 129 (1), 23-31 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Entamoeba invadens
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 686)
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Contact: Brendan Loftus
Department of Eukaryotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: enta@tigr.org
DNA was provided by Daniel Eichinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entamoeba invadens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medical Center Drive, Rockville, MD 20850,
/GD Ares Converged (Clone - MEXIVAY) (Site - 1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens IP-1 using a Qiagen plant DNA extraction kit. A shotgun medium-size plasmid library (average insert size of 10 - 12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHOS2."
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                                                                                                                                                                                                                                                                                                  strain-"IP-1"
                                                                                                                                                                                                                                                                                                                      organism="Entamoeba invadens"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                           xref="taxon:33085"
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Shiroishi,
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi,ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hpp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSM01. For BAC Clones are derived from the mouse BAC library MSM01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Kuniya Abe
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contribution of Asian mouse subspecies Mus musculus molossinus genomic constitution of strain C57BL/6J, as defined by BAC-end
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LIBRARY
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                                                                                                                                                                                              /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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                            tissue type="mixture of kidney and spleen"/clone_Tib="MSMg01 Mouse Male BAC Library"
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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81-559-81-6855
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                dev_stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                  sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="ddc45n05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:44689"
                                  GI:7841633
                                                                   1PIG
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                                                               Sus scrofa cDNA 5', mRNA sequence.
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Pred. No. 36;
3; Mismatches
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Pred. No. 40
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                                                                                                                                                                                                                                                                                                35;
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                                                                                                                                                                                                                                             571
tigr-gss-dog-17000326068677 D
genomic survey sequence.
CE130055
                                                            1 (bases 1 to 571)
Kirkness,E.F., Bafna,V., Halpern,A.L.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,
Venter,J.C.
                                                                                                                                             Canis ramilialis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Tamrasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                               Canis familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCAGCACG
Blate: 45 row: D column: 6
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 533)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J. Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing EST cluster assembly
                             The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                 CE130055.1
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   Contact: Kirkness
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida
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Library made from pooled tissue from day 11, 13, 1
and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
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Wang,W., Fras
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                                                                                                                                                                         Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 TATATCAATTAATAGGAAGAAAGGTAAAGATTGAGGAAAAAATTATCTTAAGTATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 UAGUCUUAGAGGUCUUGUAUAUUUAUACUUACCACACAAGAUGGACCGGAGCAGCC 119
                                                                                                                                                                                                             BACKWARD: M13r
Plate: 0222 row: E
Seq primer: M13r
Class: BAC ends.
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CC896465
CC896465.1 GI:33472202
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                              Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O.
85721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zes mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 673)
Yu.Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J
and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing of the maize genome Unpublished (2003)
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Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC896465 673 bp DNA linear GSS 07-AUG-2003
                                                                                                                                                                                                                                                                                                                Email: rwing@genome.arizona.edu
PCR PRimers
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Fax: 520 621 9288
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/mol_type="genomic DNA"
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/lab host="DH10B"
/clone_11b="ZMMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                       Location/Qualifiers
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HindIII; Zea mays L. ssp. mays"
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| Query M | Match 19.1%; Score 36; DB 9; Length 673; | |
| Best Lo Matches | Best Local Similarity 26.2%; Pred. No. 45; Matches 45; Conservative 42; Mismatches 85; Indels 0; Gaps 0; | |
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| Ü | 119 TATTATTATTATTATTATTATTATTATTATTATTATTAT | |
| | 71 AGAGGUCUUGUAUAUUUAUACUUACCACACAAGAUGGACCGGAGCAGCCCUCCAAUAUCU 130 | |
| Ū | 179 TTCTTTCTGCTGATTTAGGTACCTGATATTGACACAGGCTACCTTCCAATTTCC 238 | |
| | 131 AGUGUACCCUCGUGCUCGAAACAUUAAGUGGUGUUGUGCGAAAAGAAUC 182 | |
| Ü | 239 ATGCTGATATTTTGATGACTTATACATGAAATAGTGCTGGTTTTGTAGATTC 290 | |
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Search completed: December Job time: 1975.58 secs

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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Match
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17.9 54945
17.9 65485
17.9 65582
17.7 6601
17.7 600470
17.2 1410
17.1 1345
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Copyright (c) 1993 - 2005
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           US-09-270-767-2018
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US-09-949-016-13154
US-09-270-767-1354
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US-09-949-016-16932
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US-09-949-016-14341
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Compugen Ltd.
         Sequence 5136, Ap
Sequence 2041B, A
Sequence 10, Appl
Sequence 13757, A
Sequence 2904B, A
Sequence 68590, A
Sequence 96, Appl
Sequence 97, Appl
Sequence 1672, Ap
Sequence 1672, Ap
Sequence 1672, Ap
Sequence 16932, A
Sequence 16932, A
Sequence 16932, A
Sequence 16932, A
Sequence 16930, A
Sequence 16930, A
Sequence 16931, A
Sequence 16931, A
Sequence 16931, A
Sequence 114340, A
Sequence 114341, A
Sequence 114343, A
Sequence 114343, A
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US-09-270-767-5136
; Sequence 5136, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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Best Local (
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| 30.6 | 30.6 | | 30.6 | 30.6 | 30.6 | 30.6 | 30.6 | 30.8 | 30.8 | 31 | 31.2 | | | | 31.4 | 31.6 | 31.8 | r | 31.8 |
| 16.3 | 16.3 | 16.3 | 16.3 | 16.3 | 16.3 | 16.3 | 16.3 | .4 | 16.4 | 16.5 | | o | 16.7 | 16.7 | 16.7 | 16.8 | | 16.9 | 16.9 |
| 46806 251672 | 46805 | 11485 | 10320 | 9048 | 8093 | 7183 | 7183 | 227750 | 1405 | 7261 | 113967 | 113966 | 53558 | 50383 | 23167 | 3507 | 529885 | 529885 | 529885 |
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| US-09-949-002-842 US-09-949-016-17296 | US-09-949-002-585 | US-09-410-464-9 | US-09-949-016-11778 | US-08-973-273-4 | US-09-949-016-15241 | US-09-081-149-10 | US-09-081-149-9 | US-09-949-016-17175 | US-09-270-767-10838 | US-09-949-016-14780 | US-09-949-016-17051 | US-09-949-016-12277 | US-09-949-016-16616 | US-09-949-016-17600 | US-09-949-016-16836 | US-08-315-468-3 | US-09-949-016-14347 | US-09-949-016-14346 | US-09-949-016-14345 |
| Sequence 842, App Sequence 17296, A | • | Sequence 9, Appli | Sequence 11778, 1 | Sequence 4, Appli | Sequence 15241, A | Sequence 10, Appl | Sequence 9, Appli | Sequence 17175, 1 | Sequence 10838, 1 | Sequence 14780, 1 | Sequence 17051, 1 | Sequence 12277, A | Sequence 16616, i | Sequence 17600, A | Sequence 16836, i | Sequence 3, Appli | Sequence 14347, A | Sequence 14346, 1 | Sequence 14345, i |

ALIGNMENTS

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Sequence 20418, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
TITLE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5136
LENGTH: 759
TYPE: DNA
ORGANISN: Drosophila melanogaster
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US-09-270-767-20418
LENGTH: 759
TYPE: DNA
ORGANISM: Drosophila melanogaster
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RESULT 4
US-09-949-016-13757/c
; Sequence 13757, Application US/09949016
; Patent No. 6812339
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                                                                        GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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                                     NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0 13757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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CURRENT APPLICATION NUMBER: US/09/967,669
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: C. Frank
APPLICANT: Susan M
ORGANISM: Human
                              LENGTH: 65485
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ORGANISM: Homo sapiens
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Pred. No. 2.7;
23; Mismatches
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Pred. No. 0.
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US-09-949-016-29048/c
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US-09-949-016-12303
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                PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                 Sequence 29048, Application US/09949016
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GENERAL INFORMATION:
APPLICANT: VENTER, J.
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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35.9%; Pred. No. 2.9;
tive 23; Mismatches
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; SEQ ID NO 68590
; LENGTH: 601
; TYPE: DN
; ORGANISM: Human
; ORGANISM: 68590
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRETSEQ for Windows Version 4.0
SEQ ID NO 29048
LENGTH: 601
TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                        Query Match
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Best Local (
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
FULNE APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-39
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-0-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABSSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                    Local Similarity
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184
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                                                                                            244 TTTTAAAAATACAAACATAACACACACACAGTAAAGCAGTGAAGCTTCCCCTCTCAAAC 185
                                                                                                                                                                                                                                         14 UAUUAAAAUUAGGUUAAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUGCUAUAGUCUUAGA 73
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                                           GUACCCUC 141
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GTATCCCC 177
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PRIOR FILING DATE: 1997-09-03
PRIOR APPLICATION NUMBER: 60/053,344
PRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/050,359
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Matches
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Lyme Disease Vaccines
FILE REFERENCE: PB481US
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                                                                                                                                                                                                                                                              Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/US98/12718
PRIOR FILING DATE: 1998-06-18
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TYPE: DNA
ORGANISM: Human
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ORGANISM: Homo sapiens
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978 TGAGATAAAAAACATTATGTTTGATTTAAGATTGACAATAATTTTAAAATTTCAATGTT 1037
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                                                                                     ; ORGANISM: Drosophila melanogaster US-09-270-767-1072
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Best Local S
Matches 49
                                                                                                                                                            APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1072
LENGTH: 1345
TYPE: DNA
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GENERAL INFORMATION:
Query Match
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CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: PCT/US98/12718
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/057,483
PRIOR FILING DATE: 1997-09-03
PRIOR FILING DATE: 1997-09-03
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PRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR FILING DATE: 1997-07-22
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ORGANISM: Homo sapiens
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28.8%; Pred. No. 2;
tive 35; Mismatche;
    17.18;
    Score 32.2;
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 00/0414
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 17061
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Matches 54; Conservative
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TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT ETLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

INTEREM PRIOR FILING DATE: 2000-09-08

INTEREM
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US-09-949-016-16932
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US-09-949-016-17061
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; ORGANISM: Human
US-09-949-016-16932
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; LENGTH: 80595
; TYPE: DNA
; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
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US-09-078-294-3
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Patent No. 6265211
GENERAL INFORMATION:
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Matches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
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APPLICANT: Du Sart, Desiree
APPLICANT: Du Sart, Desiree
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davide Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
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                                              452 GATGTTATGTTTCCTTATACTTA 474
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                       72 GAGGUCUUGUAUAUUUAUACUUA 94
                                                                                             16.9%; Score 31.8; D
24.1%; Pred. No. 11;
7ative 31; Mismatches
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Search completed: December 22, 2005, 15:30:10 Job time : 86.0668 secs

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Result
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Maximum DB
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Copyright (c) 1993 - 2005
11422 7
11099 6
1099 6
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9 908 5
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2000 3
15 1601042 6
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5 1601042 6
1 1301 6
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7 US-10-088-750B-1
7 US-10-088-750B-2
7 US-10-088-750B-2
8 US-10-489-136-12
8 US-10-489-136-12
8 US-10-311-455-192
6 US-10-277-166-18
6 US-10-277-632-160930
1 US-10-277-632-160931
1 US-10-277-632-160931
1 US-10-277-632-160931
2 US-10-277-632-160931
3 US-09-938-842A-5166
4 US-09-938-842A-5166
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6 US-10-027-632-59064
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Compugen Ltd.
Sequence 1, Appli
Sequence 20, Appli
Sequence 22, Appli
Sequence 192, Appli
Sequence 192, Appli
Sequence 18, Appli
Sequence 649, App
Sequence 160930,
Sequence 160931,
Sequence 160931,
Sequence 160931,
Sequence 160931,
Sequence 5166, Ap
Sequence 5166, Ap
Sequence 5166, Ap
Sequence 5164, Ap
Sequence 5964, A
Sequence 5964, A
Sequence 1904, Appli
Sequence 4, Appli
Sequence 6, Appli
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| 33.2 | ا د د د | 3 . 6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.8 | 33.8 | 34 | 34 | 34 | 34 | 34 | 34.2 | 34.2 | 34.2 | 34.4 | 34.4 | 34.4 |
| 17.7 | 17.7 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 18.0 | 18.0 | 18.1 | 18.1 | 18.1 | 18.1 | 18.1 | 18.2 | 18.2 | 18.2 | 18.3 | 18.3 | 18.3 |
| 244196 | 22250 | 245531 | 54945 | 7040 | 7040 | 7040 | 7040 | 7040 | 2140405 | 2140405 | 1685 | 1685 | 1685 | 629 | 629 | 6227 | 6227 | 541 | 10480 | 5586 | 2452 |
| ထပ | л | 9 | ω | 8 | 8 | 7 | 7 | v | σ | s | 4 | 4 | 4 | σ | U | 7 | 9 | σ | σ | 7 | 4 |
| US-10-741-600-17745 | IIS-10-087-192-1309 | US-10-737-318-16 | US-09-967-669-10 | US-10-473-126-173 | US-10-480-846-13 | US-10-311-507-47 | US-10-221-714A-161 | US-10-172-086-13 | US-10-027-632-76212 | US-10-027-632-76212 | US-09-925-065A-669174 | US-09-925-065A-669173 | US-09-925-065A-669172 | US-10-027-632-208894 | US-10-027-632-208894 | US-10-240-589C-69 | US-10-311-455-1559 | US-10-029-386-4978 | US-10-311-455-2174 | US-10-240-454-52 | US-09-925-065A-75245 |
| Sequence 17745, | 1100 | Seguence 16, Appl | Sequence 10, Appl | Sequence 173, App | Sequence 13, Appl | Sequence 47, Appl | Sequence 161, App | Sequence 13, Appl | Sequence 76212, | Sequence 76212, | Sequence 669174, | Sequence 669173, | Sequence 669172, | Sequence 208894, | Sequence 208894, | Sequence 69, Appl | Sequence 1559, Ap | | Sequence 2174, Ap | Æ | Sequence 75245, I |

ALIGNMENTS

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Sequence 1, Application US/10088750B
; Publication No. US20040166486A1
; Publication No. US20040166486A1
; GENERAL INFORMATION:
APPLICANT: KANAMORI, Yasushi
iTITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 3190-015
; CURRENT APPLICATION UNMBER: US/10/088,750B
; CURRENT APPLICATION NUMBER: JP P2001-016746
; PRIOR APPLICATION NUMBER: JP P2001-016746
; PRIOR APPLICATION NUMBER: DF P2001-016746
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Sim
Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 200
TYPE: RNA
ORGANISM: Plautia Stali Intestine Virus
  181
                                       181 UCUCACUU 188
                                                                                  121
                                                                                                        121 UCCAAUAUCUAGUGUACCCUCGUGCUCGCUCAAACAUUAAGUGGUGUUGUGCGAAAAAGAA
                                                                                                                                                                 61 CUAUAGUCUUAGAGGUCUUGUAUAUUUUAUACUUACCACACAAGAUGGACCGGAGCAGCCC
                                                                                                                                                                                        61 CUAUAGUCUUAGAGGUCUUGUAUAUUUUAUACUACACACAAGAUGGACCGGAGCAGCCC
                                                                                                                                                                                                                                               h 100.0%; Score 188; DB 7; Similarity 100.0%; Pred. No: 3.8e-41; 88; Conservative 0; Mismatches 0;
                                                                                  UCCAAUAUCUAGUGUACCCUCGUGCUCGCUCAAACAUUAAGUGGUGUUGUGCGAAAAGAA
UCUCACUU 188
                                                                                                                                                                                                                                                                                                                                                                           Length 200;
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RESULT 2

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; TYPE: RNA
; ORGANISM: Himetobi P Virus
US-10-088-750B-2
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US-10-088-750B-2
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                                                                                                                              SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10088750B
Publication No. US20040166486Al
GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAWORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
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Best Local :
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SEQ ID NO 10
LENGTH: 281
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Query Match
Best Local Similarity
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: UF P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/088,750B CURRENT FILING DATE: 2002-03-20 PRIOR APPLICATION NUMBER: UP P2001-016746 PRIOR FILING DATE: 2001-01-25 PRIOR APPLICATION NUMBER: PCT/JP01/00641 PRIOR APPLICATION NUMBER: PCT/JP01/00641 PRIOR FILING DATE: 2001-01-31 NUMBER: OF SEQ ID NOS: 12
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APPLICANT: KANAWORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCCAAUAUCUAGUGUACCCUCGUGCUCGCUCAAACAUUAAGUGGUGUUGUGCGAAAAGAA 180
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  34.3%;
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Pred. No. 2.3e-39;
0; Mismatches 4;
  Score
Pred.
  No. 1
  DB 7;
.5e-07;
                   Length 199;
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US-10-311-455-192
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US-10-489-136-12
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FILE REFERENCE: 9286.30
CURRENT APPLICATION NUMBER: US/10/489,136
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: PCT/EP02/09844
PRIOR FILING DATE: 2002-09-03
PRIOR FPLICATION NUMBER: DE 101 43 238.0
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                   Sequence 192, Application US/103114:
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR TILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-66-30
PRIOR APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: IDENTIFICATION OF EUKARYOTIC INTERNAL RIBOSOME ENTRY SITE (IRES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Skulachev, Max
APPLICANT: Ivanov, Peter
APPLICANT: Gleba, Yuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Atabekov, Joseph APPLICANT: Dorokhov, Yurii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 56
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Plautia stali inetstine virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 ACCCUCGUGCUCGAAACAUUAAGUGGUGUGUGCGAAAAGAAUCUCACUU 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAU 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACCCUCGUGCUCGAAACAUUAAGUGGUGUUGUGCGAAAAGAAUCUCACUU 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AAUGUGUGAUCUGAUUAGAAGUAAG----AAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 28.2%; Score 53; DB Similarity 100.0%; Pred. No. 0.0 Similarity 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn version 3.2
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Skulachev, Maxim
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No. US20050014150A1
                                                                                                                                                                                                                                                                                                                                                        Application US/10311455
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US-10-017-161-743/c
Sequence 743, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
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US-10-311-455-192
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NUMBER OF SEQ ID NOS: 178
SEQ ID NO 18
LENGTH: 11422
TYPE: DNA
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Best Local Similarity 28.4
Matches 23; Conservative
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Publication No. US20040023230A1
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NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 192
LENGTH: 11422
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: PCT/EP01/07470
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
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DE 10043826.1
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28.4%; Pred. No. 31;
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28.4%; Pred. No. 31;
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RESULT 8
US-10-292-798-649/c
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SEQ ID NO 743
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TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION UMBER: 10/017,161
PRIOR PILING DATE: 2001-12-18
PRIOR PILING DATE: 2001-12-18
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
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CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
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                                                                                                                                                                                              LENGTH: 1099
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)..(1099)
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ORGANISM: Homo sapiens
FEATURE:
                                                      NAME/KEY: CDS
LOCATION: (201)..(556)
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LOCATION: (587)..(899)
                FEATURE:
NAME/KEY: CDS
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LOCATION: source
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                                                                                                                                                                                                                                                                               PatentIn Ver. 2.1
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(587) . . (899)
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RESULT 10
US-10-027-632-160930/c
US-10-027-632-160930, Application US/10027632
; Publication No. US20020198371A1
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; ORGANISM: Homo sapiens
US-09-925-065A-440970
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PHILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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US-09-925-065A-440970/c
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                 GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 440970
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Best Local Similarity
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Best Local S
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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APPLICATION NUMBER: US 60/218,006
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Sequence 160931, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wanny, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363
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US-10-027-632-160931/c
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PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09
  Query Match
Best Local S
Matches 36
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                                                                                                                                                                                                               SEQ ID NO 160931
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Best Local
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
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                                                                                                                                                                LENGTH: 908
TYPE: DNA
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ORGANISM: Human
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  Similarity 34.0
36; Conservative
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  18.9%; Score 35.6; D
34.0%; Pred. No. 18;
vative 26; Mismatches
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34.0%; Pred. No. 18;
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44; Indels
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Gaps

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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US-10-027-632-160930/c
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Publication No. US20030204075A9
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 160930
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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FILING DATE: 1999-11-23
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RESULT 15
US-09-938-842A-5166
; Sequence 5166, Application US/09938842A
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CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

PRIOR FILING DATE: 2001-06-22

PRIOR FILING DATE: 2001-06-22
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                           76 UCUUGUAUAUUAUACUAACCACAAGAUGGACCGGAGCAGCCCUCCAAUAUCUAGUGU 135
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Publication No. US20040009476A9

GRENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Chi, Tong
TITLE OF INVENTION: SME, AND METHODS OF USE
FILE REFERENCE: GRIP1300-3

FILE REFERENCE: GRIP1300-3

FILE REFERENCE: GRIP1300-3

FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/254,647

PRIOR FILING DATE: 2001-05-22

UNMBER OF EXQ ID NOS: 5379

SEQ ID NOS: 166

INMERS OF EXQ ID NOS: 5379

INMERS OF EXQ ID NOS:
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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US-10-750-185-58759

US-11-121-086-78

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US-10-750-185-20455

US-10-750-185-41397

US-10-750-185-61397

US-10-750-185-61557

US-11-088-727-15

US-11-088-727-15

US-11-108-389-15

US-11-108-389-19

US-11-058-727-11

US-11-058-727-53

US-11-058-727-59

US-11-058-727-59

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US-11-058-727-61

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Sequence 13327, A Sequence 58759, A Sequence 78, Appl A Sequence 44380, A Sequence 61097, A Sequence 61097, A Sequence 61097, A Sequence 61097, A Sequence 15, Appl Sequence 15, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 53, Appl Sequence 53, Appl Sequence 57, Appl Sequence 61, Appl Sequence 6
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US-10-995-561-13327

US-10-995-561-13327

Sequence 13327, Application US/10995561

; Deblication No. US20050272054A1

; GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13327

LENGTH: 244196
   RESULT 2
US-10-750-185-58759
US-10-750-185-58759; Application US/10750185
; Sequence 58759, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
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Best Local S
Matches 35
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(244196)
OTHER INFORMATION: n = A,T,C or
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US-11-108-389-53
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93, Appl

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57, Appl

61, Appl
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US-10-750-185-20455/c
, Sequence 20455, Application US/10750185
, Publication No. US20050260603A1
, GENERAL INFORMATION:
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Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                     RESULT 4
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; ORGANISM: Homo sapiens
US-11-121-086-78
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; ORGANISM: Bovine
US-10-750-185-58759
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Publication No. US20050266459A1
GENERRAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT EPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEC IN NOC. 10.55-04
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SEQ ID NO 78
LENGTH: 189993
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SEQ ID NO 58759
LENGTH: 2828
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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BATES, Stephen
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APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRA
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
SOFTWARE: Patentin version 3.1
SEQ ID NO 44380
LENGTH: 1330
TYPE: DNA
GRANISM: Bovine 19866880991643
US-10-750-185-44380
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US-10-750-185-44380/c
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US-10-750-185-20455
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APPLICANT: MMI GENO
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Publication No. US20050260603A1
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 20455
LENGTH: 600
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT FAPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
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                                                                           79 ИЗИАИМИМИНИСТИКСЕ САСАСА 104
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1 Similarity 32.6%; Pred. No. 2.9;
28; Conservative 24; Mismatches
TTGTTTCTGGAAAGTACCATATAAAA 1028
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KERR, Richard
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GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.

3-10-750-185-61097 Sequence 61097, Application US/10750185 Publication No. US20050260603A1

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; ORGANISM: Bovine
US-10-750-185-20406
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; ORGANISM: Bovine
US-10-750-185-61097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 20406
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Best Local Similarity
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR PRIOR DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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KERR, Richard
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HOLM, Tom
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                                                                                                                                                                                                          16.7%; Score 31.4; DB 6; Length 600; 35.2%; Pred. No. 3.4;
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Pred. No. 4.3;
                                                                                                                                                                      Mismatches
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APPLICANT: HOYAL-WRIGHTSON, CARCLYN R.
APPLICANT: HOYAL-WRIGHTSON, CARCLYN R.
TITLE OP INVENTION: WETHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT FILING NONDER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR PILING DATE: 2003-17-25
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-07-24
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PRIOR FILING DATE: 2003-11-25
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NAME/KEY: misc feature LOCATION: (68230)..(68230) OTHER INFORMATION: n is a,
                                                                        NAME/KEY: misc_feature
LOCATION: (52594)..(52594)
OTHER INFORMATION: n is a,
                                                                                                                              NAME/KEY: misc feature
LOCATION: (40260)..(40260)
OTHER INFORMATION: n is a,
FEATURE:
                                                                                                                                                                                                                        NAME/KEY: misc feature LOCATION: (36488)...(36488) OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (35901)...(35901)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: (29105)..(29106) OTHER INFORMATION: n is a,
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LOCATION: (28873)..(28873)
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LOCATION: (10272)..(10)
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NAME/KEY: misc feature LOCATION: (196415)..(196415 OTHER INFORMATION: n is a,
                                                       NAME/KEY: misc feature LOCATION: (195657)..(1950THER INFORMATION: n is
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LOCATION: (171395)..(171395)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc feature
LOCATION: (147527)...(147527)
OTHER INFORMATION: n is a,
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LOCATION: (147534)..(147534)
OTHER INFORMATION: n is a, c
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LOCATION: (147500)..(147500)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (147488)..(147488)
OTHER INFORMATION: n is a, c
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LOCATION: (140476)..(140476)
OTHER INFORMATION: n is a, c
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LOCATION: (138224)..(138224)
OTHER INFORMATION: n is a, c
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LOCATION: (127817)...(127817)
OTHER INFORMATION: n is a, c,
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LOCATION: (115312)..(115312)
OTHER INFORMATION: n is a, c
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OTHER INFORMATION: n is a,
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LOCATION: (113639)..(113639)
OTHER INFORMATION: n is a, c,
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LOCATION: (108762)..(108762)
OTHER INFORMATION: n is a, c
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LOCATION: (115315)..(115315)
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LOCATION: (89477)...(89477)
OTHER INFORMATION: n is a,
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LOCATION: (83514)..(83514)
OTHER INFORMATION: n is a,
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LOCATION: (70027)...(70027)
OTHER INFORMATION: n is a,
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LOCATION: (109378)..(109378)
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Query Match
Best Local S
Matches 36
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LOCATION: (250575)..(250575)
OTHER INFORMATION: n is a, c,
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LOCATION: (250079)..(250082)
OTHER INFORMATION: n is a, c
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LOCATION: (248915)..(248915)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc_feature
LOCATION: (241414)..(241414)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc feature
LOCATION: (235827)...(235827)
OTHER INFORMATION: n is a, c
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LOCATION: (231762)..(231762)
OTHER INFORMATION: n is a, c
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LOCATION: (231757)..(23175
OTHER INFORMATION: n is a,
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LOCATION: (217657)..(217657)
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NAME/KEY: misc_feature

LOCATION: (212445)..(212445)

OTHER INFORMATION: n is a, c
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NAME/KEY: misc feature
LOCATION: (217725)...(217725)
OTHER INFORMATION: n is a, c
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LOCATION: (215163)..(215163)
OTHER INFORMATION: n is a, c
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LOCATION: (212736)..(212237)
OTHER INFORMATION: n is a, c,
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LOCATION: (212455)..(212
OTHER_INFORMATION: n is
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LOCATION: (212442)..(212
OTHER_INFORMATION: n is
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LOCATION: (196417)..(196
OTHER_INFORMATION: n is
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; ORGANISM: Bovine 19866881267522
US-10-750-185-41557
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                                                                                                                                  FILE REFERENCE: 35718/287809

CURRENT APPLICATION NUMBER: US/11/058,727

CURRENT FILING DATE: 2005-02-15

PRIOR APPLICATION NUMBER: 60/391,786

PRIOR FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 60/460,787

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR APPLICATION NUMBER: 10/606,320

PRIOR FILING DATE: 2003-06-25
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SEQ ID NO 41557
LENGTH: 909
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                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1860
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MONILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
                                                                                                                   NUMBER OF SEQ ID NOS:
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TYPE: DNA ORGANISM: Bacillus thuringiensis (truncated)
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                                                                                                                                                                                                                                                                                                                                                                                                                     James K. Presnail
James F.H. Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albert L. Lu
Billy Fred McCutchen
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SEQ ID NO 15
LENGTH: 1860
TYPE: DNA
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1860)
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TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION UNMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
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US-11-108-389-15
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; LOCATION: (0)...(0)
; OTHER INFORMATION: 49PVD
US-11-058-727-15
                                                                                                                                                                                                                                                                                                          US-11-108-389-15
                                                                                                                                                     Matches
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Best Local Similarity 33.1%; Pred. No. 7.3;
                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (0)...(0) OTHER INFORMATION: 49PVD
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LOCATION: (10)...(1860)
FEATURE:
1008 TÁGTÄÄTCTTCAACAÁÄTGTATGGAACTÄÄTCAAAATCTACACAGCACTAGTACCTTTGA 1067
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1128 TTACCCTGGT 1137
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                                                                14 UAUUAAAAUUAGGUUAAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUGCUAUAGUCUUAGA 73
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Rafael Herrmann
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James K. Presnail
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                                                                                                                                             16.4%; Score 30.8; I
33.1%; Pred. No. 7.3;
tive 25; Mismatches
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TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
FURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
FORM APPLICATION NUMBER: 60/391,786
PRIOR FILLING DATE: 2002-06-26
PRIOR FILLING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILLING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
                                                                                                             US-11-108-389-19
                                                                                                                                     RESULT 13
                                        Sequence 19, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
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Sequence 19, Application US/11058727
Publication No. US20050261483A1
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NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: NGSR.N49PVD
-11-058-727-19
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      APPLICANT: Andre APPLICANT: Rona!
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NAME/KEY: CDS
LOCATION: (1)...(1863)
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TYPE: DNA
ORGANISM: Bacillus thuringiensis (mutated)
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43; Conserv
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Theodore W. Kahn
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      Andre R. Abad
Ronald D. Fl
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James F.H. Wong
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    Flannagan
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TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT ELING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
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TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR PILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
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LOCATION: (0)...(0)
OTHER INFORMATION: NGSR.N49PVD
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NAME/KEY: CDS
LOCATION: (1)...(1863)
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                                                                                                                                                                                                                   Albert L. Lu
Billy Fred McCutchen
James K. Presnail
James F.H. Wong
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Rafael Herrmann
Theodore W. Kahn
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Theodore W. Kahn
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NAME/KEY: CDS

COCATION: (1)...(2010)
FEATURE:
NAME/KEY: misc_feature
COCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
US-11-058-727-11
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR PILING DATE: 2002-06-26
PRIOR PILING DATE: 2002-06-26
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR PILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FREESEQ FOR WINDOWS VETSION 4.0
SEQ ID NO 11
ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2010)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: 1218-1A
US-11-108-389-11
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APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Presnail
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
APPLICANT: James F.H. Wong
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APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Fla
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PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2010
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APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
FILE REFERENCE: 35718/291049
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TYPE: DNA
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ORGANISM: Bacillus thuringiensis (truncated)
FEATURE:
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Rafael Herrmann
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Search completed: December 22, 2005, 16:40:56 Job time: 178.55 secs

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AC137603 Mus muscu
AC104108 Homo sapi
AC130416 Homo sapi
AC130416 Homo sapi
AC133175 Mus muscu
AC153502 Mus muscu
AC153502 Mus muscu
AC163476 Bos tauru
BD173516 Novel tra
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AC128470 Rattus no
AC128470 Rattus no
AC149872 Xenopus
AC04566 Homo sapi
AC009641 Homo sapi
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BX537270 Zebrafish
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AC098201 Rattus no
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Himetobi P virus
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187 bp RNA linear PAT 18-FEB-20
NOVEL tertiary structure having ability to accelerate translation
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WO 02061080-A/2.
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08-AUG-2002
31-JAN-2001 WO 2001JP000641
25-JAN-2001 JP 01P 016746
NOBURIKO NAKASHIMA; XASUSHI KANAMORI
C12N15/11,C12N15/86;C12P21/02
NOVEL tertiary structure having ability to accelerate translation activity
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                                             /organism="Himetobi P virus"
/mol_type="genomic RNA"
/db_xref="taxon:81583"
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Dicistroviridae; Cripavirus.

CE 1 (bases 1 to 187)

RS Nakashima, N. and Kanamori, Y.

NOVEL translational activity-promoting higher-order structure patent: JP 2002306168-A 2 22-CCT-2002;
AL Patent: JP 2002306168-A 2 22-CCTUAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES

OS Himetobi P virus
PN JP 2002306168-A/2
PD 22-CCT-2002
PF 25-JAN-2001 JP 2001016746
PF 100BUHIKO NAKASHIMA, YASUSHI KANAMORI CLINI5/09,C12R1:92) CC C12N15/09,C12R1:92) CC
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Himetobi P virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD177016
     UUCACUA 187
                                                        GCAATATCCAGGGCACCTAGGTGCAGCCTTGTAGTTTAGTGGACTTTAGGCTAAAGAAT
                                                                                                          GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAU 180
                                                                                                                                                                        TACATTTTAAGACCCTTAGTTATTTAGCTTTACCGCCCAGGATGGGGTGCAGCGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAU 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAAUGUGUGAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACATTTTTAAGACCCTTAGTTATTTAGCTTTACCGCCCAGGATGGGGTGCAGCGTTCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Himetobi P virus"
/mol_type="genomic RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism='Himetobi P virus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic RNA"
/db_xref="taxon:81583"
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 187; I
66.3%; Pred. No. 1e-1
tive 63; Mismatches
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AB017037
LOCUS
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PUBMED
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181 TTCACTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-AUG-1998) Nobuhiko Nakashima, National Institute Sericultural and Entomological Science, Department of Insect Physiolosy and Behavior; 1-2 Owashi, Tsukuba, Ibaraki 305-8634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakashima,N., Sasaki,J. and Toriyama,S.
Determining the nucleotide sequence and capu
himetobi P virus: a member of a novel group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Himetobi P virus
Viruses; ssRNA positive-strand viruses,
Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 9275)
Nakashima, N. and Sasaki, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonstructural protein precursor; Himetobi P virus
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                                                                                                                      DESMANVAQEQSSGDTWNGPLMILLMSVEGVSAGALKSARCMNAIRCISMLPRAEGGID
TIFTWIKSTYTMCYRIESKYVLGVDGGYQVSADSHPVASWLEELGEPYKSFSNGTFSY
DSATESIHSLPIRGLNLQRSESFENDDIAIRTGMDCLNKIITEFSRNIEAGSGRU
DSATESIHSLPIRGLNLQRSESFENDDIAIRTGMDCLNKIITEFSRNIEAGSGRUP
PVVIYLHGGSGVGKSTLTNVLAASILSKIQPDMNLKKQCKNLIYSRASEQEFWDGYTG
QLVTVEDDFSQRADSAGNENVELFDIVRAANVYPYLLKKAMLSDKASTNETSKIIIGS
SNLKQRYTESLNEPNALLYRREDFVSSLDEKIQEILQSTQFEDVPLNVAQEQVNCDVLG
FCNCDCWGETMCVMTNLHQPKWKQWLLKMKHYVTGIPKGSVYEAFEKNEFLSQEYLNA
SKSRFGREMLTSIKEREPVIKOLLRIHLLVATVVMGPMVFFFYSBYRVKPVRVEMSFPS
GRVGGSEMNLASIQLDLRIHLVATVVMTNLFYSBYVFFKVENDHISFPS
GRVGGSEMNLASIQLDLNYIKEYKEQGVSDQNAABICSKLVTKNMFKIYVENDHYSIPL
GHVLFIKGRIANMFHHFLAALKKFKEQHEGGVVFFRULFLSRAFFVLEDHIKKVEFF
ESPEPTESLAESRDLCSFCLDNTINFSDVSKLFVSKSDLSYLKSSDILLPTLSTPSNG
QAFAKIKIGRAAGGIQRODCRYGGSDFTDRLRLVRYCKFCQLRDTPEFSPNQYRLEK
FASPCVBUDARNLENSVASHLCKSILENGLITTPKTKFCQLRDTPEFSPNQYRLEK
FASPCVBUDARNLENSVASKSVISPSPLHGILTTPKTKFCQLRDTPEFSPNQYRLEK
FASPCVBUDARNLENSVASKSVISPSPLHGILTTPKTKFCQLRDTPEFSPNGVRLEK
FASPCVBDARNLENSVASKSVISPSPLHGILTTPKTKFCQLRDTPEFSPNGVRLEK
FASPCVBDARNLENSVASKSVISPSPLHGILTTPKTKFCQLRDTPEFSPNGVRLEK
FASPCVBDARNLENSVASKSVISPSPLHGILTTPKTKFCQLRDTPEFSPNGVRLEK
FASPCVBDARNLENSVASKSVISPSPLHGILTTPKTKRAILLRQVVBEIIQAGAIDEEEFI
NSVKRSSSPGYFFVEDKEMNSKKIFCKGREPEDVTNEKAILLRQVVBEIIGAAGGIGGST
GTNVYSYDMTIANTLLSKSEPCMIAGGDFGFDSSQLQDILAAASQULLANSRDMLGST
GEDILVMOVLLEKILSSVHANNAYVVMLKGISFGERAGVTLAAASQULLANSRDMLGST
GEDILVMOVLLEKILSSVHANNAYVVMLKGISFGERAGVTLAAASQULLANSRDMLGST
GEDILVMOVLLEKILSSVHANNAYVVMLKGISFGERAVGIDEEGTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virol. 144 (10), 2051-2058 (1999)
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TLVLSWNEVCESMSVERMVAVCECAREQGLFNVSLGINDDTKGYIDSVVSRIGNGVCS
LYTDYMLGLEVAASDILVNLKYIVGFLVAAVLVGVATYCGVKMISKLFNFFLSLVFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / translation="MSQLIQTKISSYKNYVNQKIKEGRSNIHPLIRATPNFVEDVESD
LKNILBAIRTTDVFKYVVELTIGHQDLDFGYFKLYNRDLENLYSMTSNNETHLHFD
LYNNLEYVNAENKDLDLLCGENDSMDQYVLSRQLKEMBAINVELQAGNVDFILDTVNB
DCQIALYYMTRVLYDAKVCSRRVRRTAYALCRILNHVFEHLIFYINKDLIENFELCVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol type="genomic RNA"
/specific host="Laodelphax striatellus"
/db_xref="taxon:81583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="nonstructural
/protein_id="BAA32553.1"
/db_xref="GI:3493358"
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virus genomic RNA,
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Himetobi P v
AB183472
AB183472.1
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                                                                                                          Direct Submission
Submitted (08-JUL-2004) Nobuhiko Nakashima, National Institute of
Submitted (08-JUL-2004) Nobuhiko Nakashima, National Institute of
Agrobiological Sciences, Owashi 1-2, Tsukuba, Ibaraki 305-8634,
Japan (E-mail:nakaji@affrc.go.jp, Tel:81-29-838-6109,
                                                                                                                                                                                                                                                                                                                                                                                                                     Himetobi P virus
Himetobi P virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                 2 (bases 1 to 9275)
Nakashima, N. and Noda, H.
                                                                                                                                                                                                                                                                                                                                              Nakashima, N., Kawahara, N., Spherical viruses isolated
                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                        Fax:81-29-838-6028
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LWRGSI VYTFRAVKTEVHSGR LEFSPNEF I NLDMYNTMKTTRSSYKVILDLETQTE
I SETTVPYAGTTPFEKR IR PELINELSSSGIS VDDENVFATGVLGVRALFPLVLGSTVVPS
TIQIL VEMKGEPDFEVECPNSTGMMP I HS I TPAATGRDTVDSELVSTAQEQANFASTG
QHD I RSDYLEDKI E I KOI TG I SSNI SLMTEKSLSCVGSEFGNEFDL I KREGMEKNQSV
AFTNYKI LGGI PI VNYTSSI ACTGLTLTADGGSTPLTMVSSMYAFFRGERAKVY IND
LPAGEMVQGALI DNSQNTNVPQPLALQSLQYELSDKRLYEFSMPYYCPTYLTTYPSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSPLNQVSQPNLKVNI FGYYDNVTLGYPTLGTI ALSPVAVAREQVNLNSEADMLRI AE
SRNFPTKI AAS I NGVI QKGSD I LGNVLPQTKSFTNPVAKI SDAAFDI I SMI PGFKKPD
KTNHGETVLFRPTQY FGNVDGVEHSHKLGYHAMNR I DFQPDFAGSKMDEMSFDYVKR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tranelation="annnnnnnnnsokvnntffsdrrnbysgridesveftgeit
Headnapyidssiagetnikeslytdehdrghsvisftokroliktvemapgtaggs
LLTTIDIEDLIMTSMYYDKLOGFATEKADTIERVQVNAQPFQCGRLVMAYIPMEDSLS
TRTAELTRAIDRIIALPHVQLDISEQSEVTLRVPYISPYSAYNLIEGRYEMGRVVVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="capsid protein precursor"
/protein_id="BAA32554.1"
/db_xref="GI:3493359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 upstream codon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNYISDLVNPTTYARITTISEYATAYAMAAADDFDCGFYLGAPLSWNWEIERLAGRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="translation is supposed to start at several upstream codon, directed by Internal ribosome entr
/virion
                      organism="Himetobi P
                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                               .9275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 187; DB 13 66.3%; Pred. No. 6.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
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                                                                                                                                                                                                                                                                                                                                            Omura, T. and Noda, H. from the brown planthopper, Nilaparvata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence, isolate: Izumo.
                            virus"
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JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

FEATURES

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ORIGIN

Best Loc Matches

124;

Conservative

100.0%; Score 187; DB 13; 66.3%; Pred. No. 6.3e-37; tive 63; Mismatches 0;

Indels Length

Gaps

0

9275; 0;

Query Match Best Local Similarity

REFERENCE

TITLE

RESULT 4 AB183472

VERSION

KEYWORDS ACCESSION Shoo S

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ORIGIN

Matches

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DESMMINDAGEGSEDDTWINGPLMILLMS VFGVSAGALKSARCMNAIRCISMLPRAESGID
TIFTWAIKSTYTMCYRIFSKYVLGVDGGVGVSADSHPVASWLEELGEPYKSFSNGTFSY
DSATFSIIHSLFIRGLNLQRSBSFRSBOIA RTGMOCLIKILTBEFRSRNIEAGSGYRNP
DVIIYLHGGSGVGKSTLTNVLLASILSKIQPDMNLKKOWKNLIYSRASEQBFWDGYTG
QLUTVUFDDFSQRADSACNPNVELFDIVRAANYPYDLHAMLSDKASTMFTSKIIIGS
SNLKQPKTESLNFPNALYRRFDVCVSVSKNEKYNDVVPTHFVEDFYQFQEYDMLKKED
LGSTDWEGIVSKCVELIYKHSDFVSSLDEKIQBYLGSTQFEDVPLNVAQEQVNCDVLG
FCNCDCWGEFMCVMTNLHQPKWKOWLLKMKHYVTGIPKGSVYEBAFEKNRFLSQEYLNA
SKSRFGRWLTSIKERFPVIKDLRIHLVANTVMGPMVFGVKKLFAKKNECVELHVS
ESYDVGNIKPTRTESYBTPNVEPTKTESYESPNVKSVKTESYBSBVKFVRVEWSFPS
GRVGGSEMNLASLQLDNYIKEVREQGVSDQNAABIGSKLTYKNFKIYVENDHYSIFL
GHVLFIKGRIAIMPHHFLAALKKFKEQHEGGVYFRNLFLSRAFFVKLEDMIRKVKPF
ESPEPTESLABSRDLGSFCLDNTINFSDVSKLFVSKSDLSYLKSBDILLFTLSTPSNG
QAFAKIKIGBAASGIQRQDCRYYGSDPTDRLELVRYCWRYCHTEVGDGGAPLIARNV
                                                                                                                                                                                      HFADNAPVIDSSIAGETNIKFSLVTDFHDNROHSVISFLQRPQLIKTVEWAPGTÄQGS
LLTTILD ENDLMTSMYDKLDGFATFKADTIFRVQVWAQFFQCELVWAYIFWEDSLS
TRTABLITAAIDRIIALFHVQLDISEQSEVILKYPISFYSAYNLIBGRYKMGRVVAV
YSPLNQVSQPNLKVNIFGYYDNVTLGYFTLGTIALSFVAVAREQVNLNSEADMLRIAE
SRNFFYKVAASINGVIQKGSDILGSVLFQTKSVSNFIAKISDAYDFDIISMIFGFKKPD
KTTHGBTYLVRFTQYKFGUNGVEHFKLSVLFAWNRIDFQDFAGSKMDEMSFDYVKRI
PNYIASFSYSNSNVYGDTLMTTAVSFCYRSADYTTTNGARNFSFFTFTSLTVAIGFFS
LARGSIVYTFFAAVKTEYHSGRIEFSFROHSVATHFLUGGSTVDFS
TISTTYPYAGTTFFFKAIRFEINPLSTYAGISVNDFVBTGTTASFYVKKVILDLRTQTE
ISFTYPYAGTTFFFKAIRFEINPLSTYAGISVNDFVBTGTTASFYVKKDILGASTVPS
TIQILVEMKGGFDFEVECPNSTGMMFIHSITFAATGRDTVDSELVSTAQEQANFASTG
QHD IRSDYLEDKIEIKDITGI PSNVSLNTEKSLSCVGESFONFRIFIKRFGWHKOQSF
AFSNTKI LSGIFI VNYTSNISGTGLTLTADGGSTPLTMVSSNYAFFRGGFRAKVYIHD
SLPACEMVQGALIDNSQNTMVPQFLALOSLOVELSDKRLYEFSWPYYCPTYLTTYPSGS
LNYISDLVNPTTYARITTI SEHATAYAMAAADDFDCGFYLGAPLSWNWEIERLAGRLD
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QQHVFIDTLKDERKPIHKAHKTRMFSACPLDYLIACKWYFGGVVSLLQKSRNICGISV
GTNVYSYDWTILAWTLISKSPCKIAGDFEGFBSQLQDILRAASQVLLLWSRDMIGST
EBDLLVMQVLLESLLSSVHLNNNYVYMMLKGLPSGHFLTAIINSIFVLISFSSVWQIA
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PESTSFVVLDKIEKPLYASSKSVISPSPLHGILTTPKTKPCQLRDTPEFSPMQYRLEK
FASPCVPVDARMLENSVSAVSNHLCKSILENKDLITTSDKSRYSFEEAVSGIDEEEFI
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TLVLSWNEVCESMSVERMVAVCECAREQGLFNVSLGINDDTKGYIDSVISRIGNGVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="capsid protein precursor"
/protein id="BAD27585.1"
/db xref="G115025150"
/translation="ANNNNNNNTNSQKVNDTTFSDRENPSVSAGRIDESVEFTQEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="translation starts at GCU (alanine)
directed by internal ribosome entry site"
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ATVNAPYRSLNEVSYLKRKFLWDEDKRQYLAPLSLETVLETPMWVKKCVDVNLQTTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYTDTMLGLEVAASDILVNLKYIVGFLVAAVLVGVATYCGVKMISKLFNFFLSLVFKS
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LKNLNEAIRTTNVFKNYVVELTLGHQDLDFGYFKLYNRDLENLVYSMTSMNETHLHPD
LYNNLEYVMNPNKDLDLLCGENDSWDQYVLSRQLKENRAIWVCLQAGAVDPILDTVNP
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/isolate="Izumo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/db_xref="GI:50251149"
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/country="Japan:Shimane, Izumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="nonstructural
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BD173511
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Best Local S
Matches 74
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                                                                                                                                                                                                                                                                    JOURNAL
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                              181
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WO 02061080-A/1.
Plautia stali intestine virus
Plautia stali intestine virus
Viruses; ssRNA positive-strand viruses,
Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                         HELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BD173511
Novel tertiary structure
                                                                                                                                                            Similarity
                                                                              UUCACU 186
                                            CCAATATCTÄGTGTÄCCCTCGTGCTCGCTCAAACATTAAGTGGTGTTGTGCGAAAAGAAT
                                                                                                               CTCACT
                                                                                                                            AAUGUGUGAUUJAGAAGUAAG---AAAAUUCCUAGUUAUAAUAUUUUUJAAUACUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAATATCCAGGGCACCTAGGTGCAGCCTTGTAGTTTTAGTGGACTTTAGGCTAAAGAAT 6465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUUAGUGGACUUUAAGGCUAAAGAAU
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                 translation activity
                                                                                                                                                                                             /organism="Plautia stali
/mol_type="genomic RNA"
/db_xref="taxon:64698"
                                                                                                                                                                                                                              /organism='Plautia stali
                                                                                                                                                            34.4%;
                                                                                                                                                    43; Mismatches
                                                                                                                                                           Score 64.4; DB 6;
Pred. No. 8.6e-06;
                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                               intestine
                                                                                                                                                                   DB 6;
                                                                                                                                                                    Length 188;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                    accelerate translation
                                                                                                                                                                                                                                       intestine
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JOURNAL
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VERSION
KEYWORDS
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BD177015
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                                                          said DNA.
E28980
                                                                   A30 DNA promoting translational efficiently synthesizing prot said DNA.
                                          E28980.1 GI:13020960 JP 1999290084-A/1.
1 (bases 1
Nobuhiko, N.
                           unidentified
                 unclassified
                                 unidentified
                                                                                                                                                                                                                                                                                                                                                                   Novel
Key
FT 8
                                                                                                                                                                                                                                                                                      Similarity
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JP 2002306168-A/1.
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and Jun,
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61 UACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCU 120
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PN JP 2002306168-A/1
PD 22-OCT-2002
PF 25-JAN-2001 JP 2001016746
PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02// PC (C12N15/09, C12R1:92) C12N15/09, C12R1:92) CC (C12N15/09, C12R1:
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Nakashima,N. and Kanamori,Y.
Novel translational activity-promoting higher-order structure
Patent: UP 2002306168-A 1 22-OCT-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND
ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMO
CRGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
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Plautia stali intestine virus
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CAATATCTAGTGTACCCTCGTGCTCGCTCAAACATTAAGTGGTGTTGTGCGAAAAGAAT 181
                                                                                               AAUGUGUGAUCUGAUUAGAAGUAAG---AAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.4%; Score 64.4; DB 6; ilarity 39.8%; Pred. No. 8.6e-06; Conservative 43; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism='Plautia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Plautia stali
/mol_type="genomic RNA"
/db_xref="taxon:64698"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intestine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 188;
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                                                                                                                                                                                                                                                                                                                                                                                                        61
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430 bp DNA linear nal activity into protein protein gene

PAT 18-JUN-2001 and method for with the use of

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REFERENCE
AUTHORS
                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
AB006531
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FEATURES
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PUBMED
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Best Local 8
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                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 UUÇAÇU 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 UACAUUUUUAAGACCCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCU 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-AUG-1997) Nobuhiko Nakashima, National Sericultural and Entomological Science, Department of Physiology and Behavior; 1-2 Owashi, Tsukuba, Ibaraki
                                                                                                                                                                                                                                    Sasaki, J., Nakashima, N., Saito, H. and Noda, H. An insect picorna-like virus, Plautia stali intestine virus, genes of capsid proteins in the 3' part of the genome Virology 244 (1), 50-58 (1998)
                                                                                                                                                                                                                                                                                                                                                                           Plautia stali intestine virus
Plautia stali intestine virus
Plautia stali intestine virus
Viruses, serva positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74;
                      Japan (E-mail:nakaji@nises.affrc.go.jp, Fax:81-298-38-6028)
                                                                                                                                                                2 (bases 1 to 8797)
Nakashima, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyprotein, capsid
AB006531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB006531 8797 bp Plautia stali intestine virus R
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                                                                                                                                              Direct Submission
                                                                                                                                                                                                                  9581777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB006531.1 GI:2344756
                                                                                                                                                                                                                                                                                                                                                              Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTATGTGATCTTATAAAATTAGGTTAAAATTTCGAGGTTAAAAATAGTTTTAATATTGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAATATCTAGTGTACCCTCGTGCTCGACCTCAACATTAAGTGGTGTTGTGCGAAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUUAGUGGACUUUAGGCUAAAGAAU 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATAGTCTTAGAGGTCTTGTATATTTATACTTACCACACAGATGGACCGGAGCAGCCCT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAUGUGUGAUCUGAUUAGAAGUAAG---AAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCACT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INST OF SERICULTURAL Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOBUHIKO NAKAJIMA, JUN SASAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1998 JP 1998114428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C12N15/09,C12N5/10,C12N7/00,C12P21/02//(C12N15/09,C12R1:92),
(C12N5/10,C12R1:91),(C12N7/00,C12R1:92),(C12P21/02,C12R1:91),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12N15/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L2N5/00, (C12N15/00,C12R1:91) CC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP 1999290084-A 1 26-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64.4; DB 6; Pred. No. 7.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA for nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete cds.
                                                Tel:81-298-38-6109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCIENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                  National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRL.
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                                                                       Insect
305-8634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
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S
                                                                                                                                              ORIGIN
                                                Matches
                                                                                           Query Match
                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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                                                                       Similarity
AAUGUGUGAUCUGAUUAGAAGUAAG----AAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGC
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EILSKTVCRNYYALFVCRPDGRESRLCHILFILKDKIGYMPQHFIFSLIKKEMEESPDSF
ISLRSIFLRVNMYEIYICDFLNYNIFVPENDGGRLVDSCLUDVETVTKHPDILITTYVS
GTEVKSILRSDVCLPFIHVPESNKYKFYATIAYGTGGQQLVKGGEISSITVATFYF
RQSWKYKLQTJASGTCGAPVILIGAKQPGRICGMHVMGDSQCNGYAVAITREILCKWI
UDLNFTIQSSEMEKKMIQNGVFDTLPFPGKFISLGDSPISISAASKTQLRKSVLYGEI
APVLTKPTWITPGTLMGEVMDPRNYKLSLFGRPRTLVKMNLLNSIKDRLVQRIYVMEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLDKFF11FEBSLVCQDGLKDESQFLSLFLLDKLFLNGCPVSMKNAKDFVWFVSQAPR
FSQG1TM1VSYVBDLYVHCEHFFRVKI1GLESISYESSPVCTW1EA1QD1YEKYKKNIL
VLDARLLDKLFLNLYKSGMRFLCTPAFRONGSQ1IVKY1MLTVRLIDKVP1SQRGYKNS
KRPPPVSLLLLGGTGRGKTTVTFPLTTEVATR1YLEEHEGD1TDED1ASSIYARNSEQ
EXYBGYTGQLITVFDDFMQRKUSASNENLEIFEM1RASNIFPYPLHYANLEDKNNTWF
RSSV1LASSNILTAENLQSKVHSLNYPVALLERFDLVVEVEIAPGCTKRPAGQPFKD1
KKFTKVBY1LDESDRVS1VRSEISYDEIVKLMCLKYKDNMTTCQSVSANITEMIGNVR
KQVMKAKEESHLTIESENNLLATQGWLSWFVDSYEBENDLGVDFDDEVVTPDQY1E
KFTRVID1TPDPKPDEISADKERTTMIWRTHFSQ1CEEYPIVPLATGTVTALGV
GYTIYRCFFNGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
GYTIYRCFROGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
GYTIYRCFROGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
GYTIYRCFROGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
GYTIYRCFROGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
GYTIYRCFROGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
GYTIYRCFROGSTTPLAKSEIVLPKFPESQEKEGVISRCKIESQEKLGSVSKVRVESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /6193 . 8628
/note="Either readthrough of terminal codon of orf for nonstructural polyprotein or use of int ribosome binding site. Confirmed N-terminal of protein precursor starts at 6193 by N-terminal
                                                                                                                                                                                                                                         /translation="QekeftQgrdTTaQskxipgaQagelnngveyQeQivsfsddam
KIDECLISCAAQTMMESRPAEDFREHTIVDFLERPRVATHIMSTADARNTHLVDLEI
PKALLDNMMLKFDGFSSFSATVEFKLQINSQPFQAGLLIMGALPSKDLIGSBNTDVK
VAVDKSLYIPHTLFDISKTSEITLSVBYVSPFBQYNLVLEPINWSNFFIKVYSDLVSK
QTDQLDLVLWARFKDIKLGYPTVLPVKTPTTDLILQSGETSGPVSKVAATIUDVAEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GŚNYKYĖSRYPFETACEGIDSDPTFNSIKRKTSAGYPLCSKVKNGKQBIFGSDGPFNF
KTKLALDLRKDVEHIESLAMDGISSYHVFIDTLKDERKAIEKAKTRLESAS PLPYLI
CCRWYLOGGYSRLIRGKIVNNIA VGTONPYSDDWTRVAHILLBURHFVASDEPAS VDSSO
EKBILRAACEVIVELCEDLSLPQSERDKHRRVRWVLLESLLNSVHYSYGKLYYWSKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MMFSLNSLNSRTDFTDDDLMLLDLEKPVTLFDKEIFRQTIADMDGKDSYSYSIERNIFDKHIFRQHILDMDGKDSYSYSIERNIFEDLHUPYLGNVHIVRKURFIQEIKRWYDMYNDVCVSPTSFYILGUPHEDLETSGOYNTHLLFRSDVDLVVBYBRNCVWFDLSARDVETYSFYILGLPENIQYNCLDQILDDRFTSEDLFHLIENLQFARKLPLVVFDGKWRFQQPHLSLFKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLLSRI VONYAFYRGGINIKVAPDKGOVVPNLYYAYISGLTTSSNTYNGYPFSVEQYN
AKSLCEFNYPYYNSFKFSAVATNOTVPNVTOPFFNFIAAGRVAVSAKDDFDCGFFLGP
PPSVFRPTLKTIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGVEVEFLSRHAAFQAVRETDFFEEES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSGHFLTSIINSIFVNIAMCYAFVESQEKGNRSEENIRVFFNDFSIVTYGDDHVIGVP
EKYVEDFNQLTLPKLLKTLGLDYTMEDKDRICDIKSRKLEEVTFIKRSFRYVKELDRW
LAPLDLNSILDCMNWQRSGEDEGLNAQANVSFALKELSLHPEDVWDQWFPLILRACNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Plautia stali intestine virus"
/mol type="genomic RNA"
/specific_host="Plautia stali"
/db_xref="taxon:64698"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="capsid protein precursor"
/protein ida="BAA22088.1"
/db_xref="GI:2361038"
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                                                                    34.4%;
                                           ; Score 64.4; DB 13; Pred. No. 5.2e-06; 43; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FATERITY AND FISHERIES, NOBUHIKO NAKASHIWA, YASUSHI KANAMORI
PD 08-AUG-2001
PD 08-AUG-2002

WENT OS Cricket paralysis virus
PD 08-AUG-2002
PF 31-JAN-2001 JP 015
PI NOBUHIKO NAKASHIWA, YASUSHI KANAMORI
PR 25-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 JP 015
PC C12N15/11
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WO 02061080-A/4.
Cricket paralysis virus
Cricket paral
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                                                                    GCCCTCTCTGCGGTTTTTCAGATTAGGTAGTCGAAAAACCTAAGAAATTTAC 186
                                                                                                           A-CCUAGGUGCAGCCUUGUAGUUUUAGGGACUUUAGGCUAAAGAAUUUCAC 185
                                                                                                                                                                                                  CCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGGGC 134
                                                                                                                                                                                                                                                                                       UGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCACT 6191
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                                                                                                                                                         GGTTAGCTATTTAGCTTTACGTTCCAGGATGCCTAGTGGCAGCCCCACAATATCCAGGAA
                                                                                                                                                                                                                                              TGCTTGTAAATACAATTTTGAGAGGTTAATAAATTACAAGTAGTGCTATTTTTGTATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UUCACU 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation activity
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Cricket paralysis virus"
/mol_type="genomic RNA"
/db_xref="taxon:12136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism='Cricket paralysis virus'.
                                                                                                                                                                                                                                                                                                                                                       24.88;
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                                                                                                                                                                                                                                                                                                                                  Score 46.4; DB Pred. No. 0.3; Nismatches
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having
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AF218039
LOCUS
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Matches
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Cricket paralysis virus
Viruses; seRNA posttive-strand viruses,
Dicistroviridae; Cripavirus.
  Wilson, J.E.,
                                                                                                                                                                                                                                                                                         AF218039.1 GI:8895506
                                                                                                                                                                                                                                                                                                              polyprotein genes,
AF218039
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JP 2002306168-A/4.
                                                                                                                                                                                                                                                Cricket
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                      (bases 1 to 9185)
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                                                                                                                                                                                                                    paralysis virus
paralysis virus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Cricket par
/mol_type="genomic RNA
/db_xref="taxon:12136"
    Powell, M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.8%; Score 46.4; DB 36.6%; Pred. No. 0.3; Live 37; Mismatches
                                                                                                                                                                                                                                                                                                                                  complete cds.
    Hoover, S.
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RNA"
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    and
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135 GCCCTCTCTGCGGTTTTCAGATTAGGTAGTCGAAAAACCTAAGAAATTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 GGTTÄGCTÄTTTAĞCTTTACGTTCCAĞĞATĞCCTAĞTGĞCAĞCCCCACAATATCCAĞGAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 CCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGGGC 134
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Viruses, ssRNA positive-strand viruses, no DNA stage;
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1 (bases 1 to 188)

Nakashima, N. and Kanamori, Y.

Novel translational activity-promoting higher-order structuneth: JP 2002306168-A 4 22-OCT-2002;

PATENT: JP 2002306168-A 4 22-OCT-2002;

DIRECTOR GENERAL OF NATIONAL INDUSTRIAL TECHNOLOGY EN CORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CRGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
Dicistroviridae; Cripavirus.

1 (bases 1 to 9185)
Wilson,J.E., Powell,M.J., Hoover,S.E. and Sarnow,P.
Wilson,J.E., Powell,M.J., Hoover,S.E. and Sarnow,P.
Naturally occurring dicistronic cricket paralysis v
regulated by two internal ribosome entry sites
Mol. Cell. Biol. 20 (14), 4990-4999 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF218039 9185 bp RNA linear Cricket paralysis virus nonstructural polyprotein
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C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02//:
(C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC
(C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC
NOVel translational activity-promoting higher-order structure FI
NOVEL TRANSPORTER STRUCTUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71;
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Sarnow,

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FEATURES JOURNAL

Submitted (20-DEC-1999) Microbiology & Immunology, Stanford University, 299 Campus Drive, Stanford, CA 94305, USA

ocation/Qualifiers

organism="Cricket paralysis virus"

_xref="genomic RNA" _xref="taxon:12136"

Direct Submission

Bource

CDS

codon_start=1

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                                                                                        Matches
                                                                                                                             Best Local Similarity
                                                                                                                                                                            Query Match
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    15 UGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAAUACUGCUACAUUUUUAAGAC 74
                                                                                        63,
                                                                                        Conservative
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GPSTQVIDPTVEGLIEVEVPYYNISHITPAVTIDDGTPSMEDYLKGHSPPCLLTFSPR
DSISATNHHITASFMRAPGDDFSFMYLLEVPPLVNVARA"
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EYTVMAHLED VDVQY P'GANI E'TĞNS PHZ LSI AERI ARĞD FTETEMRKLIM I HKTYLKR 
PAR I YAQAAKELKQLETINUS BSTALQĞI SEĞI, TTLSHI PVLGNI FS'TPAM I SAKAADI. 
AKLFGPS KPTVQĞKI ĞECKLRĞĞRMAN FDĞMDMSHKMALS STNE I ETKEĞLAĞTS LD 
EMDLESKVLS I PNYMDR FTWKTS DVTNIYVLMDNYVS PFKVKP YSATI I TDR FR C'THMĞYV 
ANAFTYWRĞS I YYTFK KVKTOĞYH ĞERLRI SE FI PYYNTTI STĞTDVS FTÇKI VVDLK 
TSTEVS FTVP YI ASR PWLYCIR PESSMLS KDNKDĞALMYNCVSĞI VR VEVLNQLVAAQ 
NVFSELDVI CEVSĞĞDDLEFAĞTTÇB SYVYAĞDLTLADTIK LE BERTÇĞY SÜNEDINR 
ITTĞÇSR I VAQVMĞEDOĞI FRNEĞDIĞVH PI SI DTHRI I SINMAŞ PQAMCI ĞEKI VŞIRĞ 
LI KRFĞI FÖDANTLQADĞS SEVVAP FTVTS PTKTLTS TRNYTÖPDYYYYL VAFWRĞSM
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SCIYGMLSKPITKPAHLTRTRLPNGEIVDFLMKGLKKCDTAVLDAEIVESAALDVK
OVLTQYNSMLDVNKKRFLTYEEATQGTGDDDFMKGLARQTSFGYRYEQMERKLPK
ODMMGSGEQYDFTSQRAQELRRDVEELIDNCAKGIIKDVYFVDTLKDERRPIEKVDAG
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QKMREDDESATKMIDGEFISYDEFARTICKAMKEEKEKTFHQLOMLEAYASRTVAQG
GSETSEYYDVMDETYFSNLLSQGFMAGKSLIEMERAEFASDATGENAYIEFKAYIEFKOR
GSETSEYYDVMDETYFSNLLSQGFMAGKSLIEMERAEFASDATGENAYIEFKAYIEFFER
TLTDDTITSEVGSSGDNKTQKISKRVVEVGSGDVKTTKPAKTAVEVGSSGDSKTMKN
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VPUSHFIAPMAERVELTACTRIKVCMPYHFIETLYACFENITIFSQPNCDDVI
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ORDCYESYNAPTQCGSIVCLYNKAMERKLIGMHIDGNSECHSYACPLTDGEINDG
NEUR YNNATTHOGGSIVCLYNKAMERKLIGMHIDGNSECHSYACPLTDGEINDG
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VNLSTNYLDMTTREDRIHSIKDFLSGFIIIATNLWSSSDFVEKQLYTANFPEVLISNA
MYQDKLKGFVGLRATLVVKVQVNSQFFQQGRLMLQYIFYAQYMFNRVTLINETLQGRS
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HFLKKRFVFSHQLQRTVAPLQKDVIYEMLNWTRNTIDPNEILMMNINTAFREIVYHGK
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NKVIAGDFGNFDGSLVAQFFGQSCGKSFYPWFKTFNDVNTEDGKRNLMICIGLWTHIV
HSVHSYGDNVYMWTHSQPSGNPFTVIINCLYNSMIMRIVWILLARKLAPEMQSMKKFR
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VEDLYKEGLKYSEEKI PDRD 1 ARP I TTWLF PAKSLYBEQVILLS PVKGGGBKORP I TVWL
TGBESGIGKTQMIYPLCIDILBEMGIVKPDAYKHQAYARQVETEYWDGYNGQKIVIYD
AFQLKDDKTKPNPEIFEVIRTCNTFPQHLHMAALQDKNMYSQAEVLLYTTNQFQVQLE
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LLVLVRLLMVWKKYRAALIVIILFVMHFYGFDKQILDIVLDLKDKILQTTTQAGTETL
EBVVYHPWFDTCGKLIFAVLAFFAIKKIPGKQDWDNYISRLDRIPKAIEGSKKIVDYC
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SKPQLLDLESECYCMDDFDCGCDRIKREEELRKLIFLTSDVYGYNFEEWKGLVWKFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="structural polyprotein"
/protein_id="AAF80999.1"
/db_xref="GI:8895508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEYQKLRSGIEDLAMKGILPQQPQILTFKAYLWDATMLADEVYDF"
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/protein_id="AAF80998.1"
/db_xref="GI:8895507"
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                                                                                                                                  24.8%;
36.6%;
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                                                                                                                             Score 46.4; DB 13; Pred. No. 0.18;
                                                                                   Mismatches
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choppelly, Collymore, A., Cooke, P., Corum, B., Chang, J., Chang, J., Changely, Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, M., Hafez, N., Galagan, J., Horton, E., Hulme, W., Iliev, I., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McClarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubba, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zinmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6043 TGCTTGTAAATACAATTTTGAGAGGTTAATAAATTACAAGTAGTGCTATTTTTGTATTTA 6102
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Submitted (10-MAY-2005) Broad Institute of MIT and Submitted (20-MAY-2005) Broad Institute (20-MAY-
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Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
Bloom,T., Boguslavkly,L., Boukhgalter,B., Camarata,J., Chang,J.,
Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC161224 160056 bp DNA linear HTG 10-MAY-: Mus musculus chromosome 5 clone RP23-32L14 map 5, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mus musculus chromosome 5, clone RP23-32L14
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 75 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L32200
Center clone name: 32_L_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www-seq.wi.mit.edu
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| Score 4 Pred. N 22; Misn | gap of u | gap of u | | | | μğ | G, | i H | contig o | | | | | | | | | | | | | | contig of | | | | gap of u | | | | | contig | contig of | | | | | | | iu r | חש |
| re 40.2; DB d. No. 4.6; Mismatches | unknown | unknown | unknown | of 3640 l | | | | | | | or 3007 I | | nown | of 1781 l | | | uwour | unknown of 1651 | | of 2579 I unknown | cnown | unknown : | | | | | unknown | nown | known | unknown . of 1838 l | | | of 2622 I | thom i | unknown of 1995 l | of 1995 l | of 2995 I | unknown | unknown of 2570 l | of 2713 l | or 1757 |
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AC131732
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                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 210499 bases at least Q40
Consensus quality: 210754 bases at least Q30
Consensus quality: 210991 bases at least Q30
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Sequencing vector: plasmid; 100%
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On May 25, 2004 this sequence version replaced gi:22758576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-AUG-2002) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 212284) Wilson, R.K.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: submissions@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of Mus musculus clone
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                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                   Location/Qualifiers
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                                 10018: contig of 10018 bp in length
10118: gap of unknown length
46629: contig of 36511 bp in length
46729: gap of unknown length
94280: contig of 47551 bp in length
94380: gap of unknown length
212244: contig of 117904 bp in length
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AC157478
                                                                                                                     MO 63108, USA
On Aug 9, 2005 this sequence version replaced gi:59858791.
                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 229783)
Zheng,X., Cotton,M., Kozlowicz,A., Haglund,K. and
The sequence of Mus musculus BAC clone RP23-33K19
Unpublished (2001)
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                                                                                                                                                                                                                                 Wilson, R.K.
Direct Submission
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Parkway, St. Louis, MO (
3 (bases 1 to 229783)
                                                                                                                                                                                           Submitted (09-AUG-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                       Contact: submissions@watson.wustl.edu
                                                                                 Web site: http://genome.wustl.edu
                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                       Center project
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="15"
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94381. .212284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:71980388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.5%; Score 40.2; DB 14; 41.2%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .46629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229783 bp
RP23-33K19
                                                                                                                                                                                                                                                                                         Genome Sequencing Center, 4444 Forest Park 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear Ruchromosome 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 212284;
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Cordum, H.

Louis,

ROD 09-AUG-2005 complete

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ACCESSION
                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                      197431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197491 TGGATTTTAAAAATATACTCAAGGTAAATCTTGAAGAAACTGTGTCATGTAGCTTTATCG 197432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinuclectide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,
                                                                                                                                                                                                        Danio rerio chromosome 15 clone CH211-147F13, WORKING DRAFT SEQUENCE, 8 unordered pieces.
CR84B749
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                 HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                CR848749.4 GI:71534791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the entire insert of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  minimal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cccaegauegeguecaeceuuccue 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCG
                                                                                                                                                                                                                                                                                                                                                                                                                TCCAGGATGGGCTGCAGAGTTTATG 197407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP23-33K19"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .229783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.2; D
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                    164647 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA"
                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 229783;
                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                    HTG 31-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 160713 bases at least Q40
Consensus quality: 161321 bases at least Q30
Consensus quality: 161959 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-helpssanger.ac.uk Clone requests: http://www.sanger.ac.uk/Projects/D rerio/faqs.shtml#dataeight On Jul 31, 2005 this sequence version replaced gi:54306004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 163947; sum-of-contigs
Insert size: 163403; 7.2% error; agarose-fp
Quality coverage: 7.21x in Q20 bases; sum-of-contigs Quality
coverage: 7.87x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: zC147F13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-JUL-2005) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McLaren, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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128468
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48102
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___ аввеmbly_fragment:00043
fragment_chain:2"
                                                                                                                                                                                                                                                                                                         vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 128367: contig of 75747 bp in length bg 128467: gap of 100 bp 128467: gap of 100 bp 149069: contig of 20602 bp in length 149169: gap of 100 bp 164647: contig of 15478 bn 4- vcation/Qualifica-
                                                                                                                                                    fragment_
                                                                                                                                                                                                                                                                                                                                                                  rragment
                                                                                                                                                    /note="assembly_fragment:00141
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                                                                                                                                                                                                                                ragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic un
/db_xref="taxon:7955"
                                                                                            note="assembly_fragment:00025"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="CH211-147F13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27092: gap of 100 bp
45046: contig of 17954 bp in length
45146: gap of 100 bp
48001: contig of 2855 bp in length
48101: gap of 100 bp
52520: contig of 4419 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type="genomic
                                                                                                                                                                                                                                                                                                                                       end:SP6
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5064: gap of 100 bp
50992: contig of 21928 bp in length
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                                                                                                                               .4800
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FEATURES

CR848749

KEYWORDS

VERSION

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Minimum DB :
Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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1: geneseqn1980
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187
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                                                                                                                                                                                                                                                                                                                                                                                                              4996997 segs, 3332346308 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Res

| Bult No. | Score | Query Match | Query Match Length | DB |) | iption |
|-------------|-------|----------------|-----------------------|----|------------|--------------------|
| ۲ | 187 | 100.0 | 187 | 8 | ABZ80708 | Abz80708 Himetobi |
| N | 187 | 100.0 | 199 | 6 | AAL50545 | Aal50545 Himetobi |
| w | 64.4 | 34.4 | 188 | œ | ABZ80707 | Abz80707 Plautia s |
| 4 | 64.4 | 34.4 | 197 | თ | AAL50556 | Aal50556 CrPV-like |
| ហ | 64.4 | 34.4 | 200 | σ | AAL50544 | Aal50544 Plautia s |
| თ | 64.4 | 34.4 | 430 | w | AAZ35832 | Aaz35832 Plautia s |
| 7 | 63.8 | 34.1 | 281 | σ | AAL50551 | Aal50551 CrPV-like |
| 80 | 46.4 | 24.8 | 188 | œ | ABZ80710 | Abz80710 Cricket p |
| 9 | 46.4 | 24.8 | | თ | AAL50547 | Aal50547 Cricket p |
| 10 | 37 | 19.8 | 190 | в | ABZ80712 | Abz80712 Black que |
| 11 | 37 | 19.8 | 202 | σ | AAL50549 | Aal50549 Black que |
| 12 | 36 | 19.3 | 189 | œ | ABZ80709 | Abz80709 Drosophil |
| 13 | 36 | 19.3 | 201 | σ | AAL50546 | Aal50546 Drosophil |
| 14 | 34.6 | 18.5 | 110000 | 13 | ABD32780_1 | Continuation (2 of |
| 15 | 33.8 | 18.1 | 300000 | 10 | ADE86352 | Ade86352 Human PTP |
| 16 | 33.8 | 18.1 | 300001 | 12 | ADO14076 | Ado14076 Human pro |
| 17 | 33.4 | 17.9 | 510 | 13 | ADQ54170 | Adq54170 Novel can |
| 18 | 33.4 | 17.9 | 190000 | 10 | ADL13752 | Adl13752 Osteoarth |
| 19 | 33.2 | 17.8 | 110000 | 11 | ACN44014_1 | Continuation (2 of |
| | | | | | | |

a a

The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

WPI; 2003-403230/38.

Nakashima N,

Shibuya N,

Nishikawa

ß

(NAAG-) NAT INST AGROBIOLOGICAL SCI. (WAKE-) WAKENYAKU KK.

Claim 1; Page 32; 39pp; Japanese.

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | | c 28 | 27 | 26 | c 25 | c 24 | 23 | 22 | c 21 | c 20 |
|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|
| 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.6 | 32.8 | 32.8 | 33 | 33 |
| 17:2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.4 | 17.5 | 17.5 | 17.6 | 17.6 |
| 450 | 450 | 450 | . 450 | 450 | 187 | 154 | 154 | 154 | 154 | 154 | 154 | 154 | 154 | 46951 | 26493 | 3660 | 2792 | 2000 | 731 | 601 | 349981 | 2714 | 2714 | 2655 | 861 |
| 4 | 4. | 4. | 4. | 4. | ω | σ | 4. | 4. | 4. | 4, | 4 | 4 | 4. | 10 | 12 | 4 | 4 | H | .4 | σ | 10 | 13 | 13 | 4 | 10 |
| AAK33250 | ABA27994 | AAI39045 | ABA59254 | AAI16383 | AAC05603 | ABS20511 | ABS45919 | AAK20141 | AAK46200 | ABA37854 | AAI52107 | ABA71772 | AAI25563 | ADE13891 | ADJ12386 | ABL26664 | ABL19920 | ACL35363 | AAL02045 | ABN63038 | ADC87619 | ADP54371 | ADR25713 | ABL13062 | ADF00812 |
| Aak33250 Human bon | Aba27994 Probe #64 | Aai39045 Probe #77 | Human | Aai16383 Probe #63 | Human | Abs20511 Human gen | Abs45919 Human liv | Aak20141 Human bra | Aak46200 Human bon | Probe | Probe | | Aai25563 Probe #15 | μ | Adj12386 DNA fragm | | Abl19920 Drosophil | Acl35363 Rice stre | Aal02045 Human rep | Abn63038 Human can | Adc87619 Human GPC | Adp54371 Human PRO | | | Adf00812 Bacterial |

ALIGNMENTS

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Himetobi P virus.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 187;
                                                                                                                            Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                                                                                                                                                                                                                                                                              CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function; protein synthesis; structural analysis.
                                                                                                                                                                                                   Nakashima N,
                                                                                                                                                                                                                                                 25-JAN-2001;
                                                                                                                                                                                                                                                                      31-JAN-2001; 2001WO-JP000641.
                                                                                                                                                                                                                                                                                                                                          Himetobi P virus.
                                                                                                                                                                                                                                                                                              08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the himetobi P virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL50545;
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                                                                                                                                                                                                                          (NAAG-) NAT
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                                                                                              Fig 1-2; 38pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; RNA; 199
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Pred. No. 4.7e-45;
Mismatches 0
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The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in producing drugs.

rch of protein synthesis and structural analysis technique. The present nucleotide represents a

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the gene

producing drugs. 1 basic research of

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RESULT 3
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Best Local S
                                      The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the plautia stali intestine virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is
                                                                                                                                                                                                                                                                                                                                            Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translativity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                  Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakashima
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Pred. No. 4.8e-45;
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          misc_binding
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                                                                                                                                                                                                                              misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CrPV-like virus-related RNA sequence
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                                                                                       stem_loop
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           /bound_moiety= "
/note= "Forms a
of itself"
138. .142
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                                                                                       80. .91
/*tag= f
97. .135
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/note= "Forms a
of itself"
                                                                  /*tag= g
107. .110
                                                                                                                                                                                            /*tag= d
/bound_moiety=
/note= "Forms a
                                                                                                                                                                                                                                       /bound moiety= "CrPV-like virus-related RNA sequence #6"
/note= "Forms a double-stranded region with bases 142-138
of itself"
                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                         *tag=
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Pred. No. 5.3e-09;
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                                  "CrPV-like virus-related RNA sequence #6" double-stranded region with bases 77-74
                                                                                                                                     "CrPV-like virus-related double-stranded region v
                                                                                                                                                                                           "CrPV-like virus-related double-stranded region v
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with
                                                                                                                                      d RNA
with
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                                                                                                                                     sequence #6"
bases 110-107
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                                                                                                                                                                                                                                                                                                                                           Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                   Sequence 197 BP; 64 A; 34 C; 36 G; 0 T; 63 U; 0
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                      GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAAGGCUAAAGAAU
                                                                   nacannunaagacccunagunaunagcunnaccgcccagganggggugcagcgcunccu
    CCAAUAUCUAGUGUACCCUCGUGCUCGCUCAAACAUUAAGUGGUGUUGUGCGAAAAGAAU
                                               UAUAGUCUUAGAGGUCUUGUAUAUUUAUACUUACCACACAAGAUGGACCGGAGCAGCCCU
                                                                                                          AAUGUGUGAUCUGAUUAGAAGUAAG---AAAAUUCCUAGUUAUAAUAAUAGUUAUAAUAACUGC
                                                                                           ACUAUGUGAUCUUAUUAAAAUUAGGUUAAAUUUCGAGGUUAAAAUAGUUUUAAUAUUGC
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184. .188
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171. .174
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/note=""Forms a double-stranded region with bases 39-35
of itself"
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/note= "Forms a
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Pred. No. 5.4e-09;
0; Mismatches 66;
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a double-stranded region with
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with
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bases 174-171
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bases 163-159
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bases 149-146
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bases 188-184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application in drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 34.4%;
Local Similarity 62.9%;
nes 117; Conservative
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                                                        UUCACU 186
                                                                                                                                                                                                                                                                                         UACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCU
CUCACU 187
                                                                                                                        CCAAUAUCUAGUGUACCCUCGUGCUCGAAACAUUAAGUGGUGUUGUGCGAAAAGAAU
                                                                                                                                                                                 GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUUAGUGGACUUUAGGCUAAAGAAU 180
                                                                                                                                                                                                                                                UAUAGUCUUAGAGGUCUUGUAUAUUUUAUACUUACCACACAAGAUGGACCGGAGCAGCCCU
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                                                                                                                                                                                                                                                                                                                                                                                                           AAUGUGUGAUCUGAUUAGAAGUAAG----AAAAUUCCUAGUUAUAAUAUUUUUAAUACUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INST AGROBIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 A; 34 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64.4; DB 6;
Pred. No. 5.4e-09;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 G; 0 T; 63 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Plautia stali intestine virus (PSIV) CC translation promoting sequence. Also described in the present invention CC are: (a) a plasmid having a gene for synthesising the objective protein CC downstream of the above DNA base sequence; (b) a plasmid in which the CC translation starting point of the objective gene; (c) a transformant in CC which the above plasmid is introduced to a host cell, a recombinant CC downstream of the above DNA base sequence; (d) a recombinant CC downstream of the above DNA base sequence; (d) a recombinant baculovirus constituted to the translation starting point of the objective gene; (e) a cultured cell infected by the above recombinant baculovirus; and (f) a combined downstream by taking a DNA corresponding to a base sequence positioned downstream by taking a DNA corresponding to a base sequence constituted a plasmid. The translation activating DNA is used for contraining the above translation activating DNA is used for
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A DNA promoting translation activity to a protein - a protein efficiently from a protein gene by using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ35832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 430 BP; 131 A; 80 C; 93 G; 126 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesising the encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-016983/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plautia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                   121
            181 UUÇAÇU 186
                                                                                                                                                                                               296 TATAGTCTTAGAGGTCTTGTATATTTATACTTACCACACAGATGGACCGGAGCAGCCCT
                                                                                                                                                                                                                                                                                                                  236 ACTATGTGATCTTATTAAAATTÄGGTTAAATTTCGAGGTTAAAAATAGTTTTAATATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Page 2; 5pp; Japanese
                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NORINSUISANSHO
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                                                                                                                                GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUUAGGCUAAAGAAU
                                                                        CCAATATCTAGTGTACCCTCGTGCTCGCTCAAACATTAAGTGGTGTTGTGCGAAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                        AAUGUGUGAUCUGAUUAGAAGUAAG---AAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.4%; Score
39.8%; Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.4;
No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 430;
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e DNA.
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                                                                                                      The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents an RNA sequence that was used in an example of the invention
                                                                                                                                                                                                                                          Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CrPV-like virus; drug production;
                                                                                    Sequence
                                                                                                                                                                                                           Example 1; Fig 3; 38pp; Japanese.
                                                                                                                                                                                                                                                                                        WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                              Nakashima N,
                                                                                                                                                                                                                                                                                                                                                          25-JAN-2001; 2001JP-00016746
                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2001; 2001WO-JP000641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein synthesis; structural analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CrPV-like virus-related RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL50551;
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                                                                                                                                                                                                                                                                                                                                   (NAAG-) NAT INST AGROBIOLOGICAL
121
                   6
                                                    Similarity
UAAUAAAAGUUUUUAAUAUUGCUAUAGUCUUAGAGGUCUUGUAUAUUUUAUACUUACCACAC
             281 BP;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
37. 71
                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
177. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; higher-order structure; drug translational activity-promoting
                                                                                    89 A; 52 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .148
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 269
                                                  34.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .215
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                                         <u>.</u>
                                        Score 63.8; DB 6;
Pred. No. 8.9e-09;
0; Mismatches 52;
                                                                                   57 G; 0 T; 83 U; 0 Other;
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                                                              Length 281;
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function;
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RESULT 8
ABZ80710
ID ABZ8
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AC ABZ8
XX ABZ8
XX ABZ8
XX ABZ8
XX Pseu
KW Pseu
KW Albu
CC CX
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                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Cricket paralysis virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudoknot; secondary structure; cell-free protein synthesis; wheatgerm; albumen; impurity; higher-order structure; intergenic region; IGR-IRES; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 188 BP; 56 A; 33 C; 36 G; 0 T; 63 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 33; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-2002; 2002WO-JP010447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ80710 standard; RNA; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing useful proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2001; 2001JP-00319923.
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                                                                                                                                                                                                                                                                                                                             100;
                                                                                                                           75
                                                                                                                                                                                                                                      15 UGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUUAAGAC
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUA 159
   A-CCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAUUUUCAC 185
                                                                                                                           ccuuaguuauuuagcuuuaccecccaagaugeeguecagceuuccuecaauauccageec 134
                                                                                                                                                                                              UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUGGACUUUAGGCUAAAGAAUUUCACU 186
                                                               GGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAA
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibuya N,
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Pred. No. 0.001;
0; Mismatches 71; Indels
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Best Local S
Matches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CrPV-like virus; 88; higher-order structure; drug development; drug production; translational activity-promoting function; protein synthesis; structural analysis.
                    ABZ80712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                  paralysis virus RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1-2; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in drugs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2001; 2001JP-00016746.
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100; Conserv
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                    standard; RNA;
                                                                                                                    A-CCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAUUUCAC 185
                                                                                                                                                                            CCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGGGC 134
                                                                                                                                                                                                                                                                                                                      200 BP; 60 A; 36 C; 37 G; 0 T; 67 U; 0 Other;
                                                                                           GCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC
                                                                                                                                                 GGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAA
                                                                                                                                                                                                          UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUA
                                                                                                                                                                                                                                   UGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCUCUCUGCGGUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC 186
                                                                                                                                                                                                                                                                Conservative
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                    ВP
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                                                                                                                                                                                                                                                                             Score 46.4;
Pred. No. 0.
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                                                                                                                                                                                                                                                                ed. No. 0.0011;
Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                    the invention
                                                                                                                                                                                                                                                                                         DB 6;
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AAL50549, AAL50549

standard;

RNA;

202

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RESULT 11
AAL50549
ID AAL50
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AC AAL50
XX
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Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Black queen-cell virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in productor weeful extensions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudoknot; secondary structure; cell-free protein synthesis; wheatgerm; albumen; impurity; higher-order structure; intergenic region; IGR-IRES; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 190 BP; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 34; 39pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                          64 AUUGUUGGAAUCACCGUACCUÁUUUAGGUUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCU
                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                   UUUCACU 186
                                                                                                                                                                                                                                                                                 AUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAA
                                                                                                                                                                                                                                                                                                                              UGCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAA 179
                                                                                                                                                                                     UUUACCU
                                                                                                                                                                                                                                                                                                                                                                                                                        ACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAU--GGGGUGCAGCGUUCC
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                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 36 C;
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Pred. No. 0.61
0; Mismatches
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07-AUG-2003 19-DEC-2002

(revised) (first entry)

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ABZ80709
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AC ABZ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
               15-OCT-2003
                                           ABZ80709;
                                                                    ABZ80709
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 202 BP; 63 A; 38 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1-2; 38pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein synthesis; structural analysis
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                                                                                                                                                                                                                                                                                                                                                               100;
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                                                                                                                                                                                                                                                                   ACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAU--GGGGUGCAGCGUUCC 119
                                                                                                                                                                                                                       UGCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUUAGGCUAAAGAA 179
                                                                                                                                                                                                                                                                                                                                  AAAAUGUGUGAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCU
                                                                    standard;
                                                                                                                                        UUUACCU
                                                                                                                                                                UUUCACU 186
                                                                                                                                                                                             AUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAA
                                                                                                                                                                                                                                                   AUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCU
                                                                                                                                                                                                                                                                                                          ACAAUGUGAUCUUGCUUGCGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell virus.
                                                                                                                                                                                                                                                                                                                                                               Conservative
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               (first entry)
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                                                                                                                                        190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; higher-order structure; drug development;
translational activity-promoting function;
                                                                    RNA;
                                                                                                                                                                                                                                                                                                                                                                           19.8%;
                                                                     189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Japanese.
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                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 6
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                     42 G; 0 T; 59 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         Length 202
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RESULT 13
AAL50546
ID AAL50
XX AAL50
XX AAL50
XX Drosc
XX Drosc
XX CrPV-
KW CrPV-
KW CrPV-
KW CrPV-
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Drosophila C virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                            CrPV-like virus; ss; higher-order structure; drug drug production; translational activity-promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translativity and function promotion, for producing useful proteins.
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                                                                                      Drosophila C virus.
                                                                                                                                                protein
                                                                                                                                                                                                                                                                  Drosophila C virus RNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 32; 39pp; Japanese.
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                                                                                                                                                synthesis; structural analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Drosophila C virus RNA sequence of the invention
                     ADE86352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                               ADE86352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises seven RNA sequences (CrPV-like viruses) which
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ilarity 58.3%;
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                                                                                                                                                                                                                                      Sequence 300000 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing and treating Noonan syndrome in a subject using a mutation a protein tyrosine phosphatase 11 gene with increased expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gelb BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; SEQ ID NO 33; 262pp; English
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37.7%;
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| | TITLE JOURNAL COMMENT | VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS | RESULT 1 AV333583 LOCUS DEFINITION ACCESSION |
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| Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itch,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. | Pukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, T., Itch, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, K., Shibata, Y., Shigamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata, Y., Shizaki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Yosunda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshina, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTB (Konno, H., et al. 1999) Unpublished (1999) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute | AV333583.1 GI:6373635 EST. Mus musculus (house mouse) Mus musculus Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 261) Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., | AV333583 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330548J20 3', mRNA seguence. |

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KEYWORDS
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Xenopus tropicalis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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                                                        1 (bases 1 to 920)

Kremitzki,C., Carter,J., McPherson,J., Warren,W.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                           CL076817 920 bp DNA linear GSS 31-DEC-2003 CH216-140K14 RM1.1 CH216 Xenopus tropicalis genomic clone CH216-140K14, genomic survey sequence.
CL076817
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                            Contact: Richard K Wilsor
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Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="medulla oblongata"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RKEN full-length enriched, adult male medulla
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CE747951/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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tigr-gas-dog-17000369575344 Dog Library Canis familiaria
genomic survey sequence.
CE747951
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Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                         Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kirkness EF
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
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                                                                                                                                                                                                       ekirknes@tigr.org
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
                                                                                                                                                  location/Qualifiers
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/clone_lib="C416"
/octone="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
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/mol type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8354"
/clone="CH216-140K14"
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1 (bases 1 to 1106)
1 (bases 1 to 1106)
1 (Kingsley, D., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M. Expressed sequence tags from Gasterosteus aculeatus Unpublished (2004)
Contact: Grimwood, Jane
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CH213-8P15.SP6 CH213 Gasterosteus aculeatus genomic clone CH213-8P15.SP6 CH213 Gasterosteus aculeatus genomic clone CL641258
CL641258
CL641258.1 GI:49660682
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanford Human Genome Center
Stanford University School of Medicine
975 S California Avenue, Palo Alto, CA
Tel: 650 320 5917
Pax: 650 320 5801
                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 21
High quality sequence stop: 737.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jane@shgc.stanford.edu
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 Conservative
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/note="Site_1: BstXI; Libraries were prepared
peripheral blood"
                                                                                                      /note="Weetcor: pTARBAC2.1; Site 1: EcoRI; The sequence of Inche "Tector: pTARBAC2.1; Site 1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center; funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (http://cegs.stanford.edu). The clone was isolated from the BAC library CHORI-213 built by Pieter deJong in collaboration with the Stanford Genome Evolution Center (http://www.chori.org/bacpac/). Clones may be purchased from BACPAC Resources in formation ben's "Technol (March 1997)".
                                                                                                                                                                                                                                                                                /clone
                                                                                                                                                                                                                                                                                                                 /sex="Mixed"
                                                                                                                                                                                                                                                                                                                                                                     mol_type="genomic DNA"
strain="Salmon River"
                                                                                         (http://www.chori.org/bacpac/ordering_information.htm)."
                                                                                                                                                                                                                                                                                                                                     clone="CH213-8F15"
                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                            organism="Gasterosteus aculeatus"
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                 19.8%;
                                                                                                                                                                                                                                                                            type="Blood"
e_lib="CH213"
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 Score 37; DB
Pred. No. 21;
26; Mismatches
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                                    DB 10; Length 1106;
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BZ349373/c
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KEYWORDS
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                                                                                                                                                                      Best Local Similarity
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471 TGCTTCCAAAGGCCCTAAGTTGCCAATATATATACACCCGTCTTGGGTCCAGCAACTCAG
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                                                             62 АСАUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mccombie@cshl.org
Plate: hq90 row: h column:
Seq primer: -21M13UnivRev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimentc Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R., Genomic shotgun sequences from Sorghum bicolor (methyl-fil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilioppida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 567)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 516 367 8884
Fax: 516 367 8874
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                                                                                                                          AAAAATTTAAGACGCTTGTCTGCATTGTTTTGACAGGACACGTTGGGAGGAGGCTTTGATG 561
                                                                                                                                                                                           AAAAUGUGUGAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCU 61
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                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="UMN107 or DH5a"
/clone lib="WGS-Sbicolorf (JM107 adapted methyl filtered)"
/clone lib="WGS-Sbicolorf (JM107 adapted methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was
digested with XbaI and one-nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
b/g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="hq90h10"
                                                                                                                                                                                                                                                                                          19.7%; Score 36.8; 1
35.2%; Pred. No. 22;
                                                                                                                                                                                                                                                        26; Mismatches
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                                                                                                                                                                                                                                                               57; Indels
                                                                                                                                                                                                                                                                                                                         Length 567;
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REFERENCE
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CL043477
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SOURCE
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Best Local S
Matches 39
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                                                                                                                                                                                                                                                                        676 TGATTTCAAATAAAAAATTATCAATTACAAAGTTTGAGTAACTTCTTGAGATATACAAC 617
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            Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                   genomic survey sequence.
CL043477
CL043477.1 GI:4049390
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CH216-57L9_RM1.1 CH216 Xenopus
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 Frelinghuysen Road, Piscataway, Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Bharti, A.K.
Dr.Joachim Messing's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bron Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003b) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZMMBBc0547L03r
                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                                                                      lone="ZMMBBc0547L03"
ab_host="E. coli DH10B"
lone_lib="ZMMBBc"
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26; Mismatches
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lone CH216-57L9,
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ORGANISM
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81 UUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAA 124
                                                                    Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MN518893 Clone ID: GQ0123_E15 Clones available through: John MacK87, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus trichocarpa x Populus deltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Coside; euroside I; Malpighiales; Salicaceae; Salicacea; Populus.
                                                                                                                                                                                                                                                      Pavillon Charles-Eugene Marchand, Quebec, Quebec, Fax: 418 656 7493
                                                                                                                                                                                                                                                                                                                                                                               Arborea EST sequencing in 
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Retzel, E. and MacKay, J.
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clone GQ0123_E
                                                       Plate: 3
                                                                                                                                                                                                                                                                                                        Universite Laval
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                                                                                                                                                                                                                                                                                                                                                          Contact: John MacKay
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Insert Length: 175000 Std Error: 0
Seq primer: RM1 TACGACTCACTATAGGGAGA
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Washington University School of Medicine
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A physical map of the xenopus tropicalis genome Unpublished (2003)
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quality sequence stop: 520
Location/Qualifiers
                                                                                                                                                                                                                              jmackay@rsvs.ulaval.ca
Location/Qualifiers
                                                    row: 15
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/clone_lib="CH216"
/notee="Vector: pTARBAC2.1; CHORI-216 X/
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus tropicalis"
/mal_type="genomic DNA"
/strain="Wilgerian frog"
/db_xref="taxon:8364"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="CH216-57L9"
                          T3 Primer.
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_E15 5', mRNA sequence.
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Pred. No. 23;
31; Mismatches
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The repetitive landscape of the chicken genome Genome Res. 15 (1), 126-136 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GL279525 378 bp DNA linear GSS 08-F Ggal_93c_PR_G02 Ggal_PR-1 Gallus gallus genomic clone Ggal_93c_PR_G02 similar to contains low-complexity sequence, genomic survey sequence.

CL279525 GSS.
                                                                     Email: paterson@uga.edu
Sequence from middle repetitive (MR) Co
Class: Hydroxyspatite-fractionated DNA.
Location/Qualifiers
                                                                                                                                                                                                              Contact: Paterson AH
Plant Genome Mapping Laboratory
University of Georgia, Center for Applied Genetic Technologies
Riverbend Research Laboratory, Room 162, 110 Riverbend Road,
                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1. (bases 1 to 378)
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Gallus gallus
                                                                                                                                                           Fax: 7065830160
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/clone lib="GQ012"
/note="Organ: Shoot apex, primary stem and developing
/note="Organ: Shoot apex, primary stem and developing
/note="Organ: Shoot apex, primary stem and developing
leaves up to and including LPI 1; Vector: pBluescript II
SK (+) XR; Site_1: Eco-RI; Site_2: Xho-I; Actively growing
shoot tips of trees subjected to fertilization with 0 or
25 mM ammonium nitrate for 1, 3, or 7 days, or removal of
a ring of bark from the main stem (stem girdling) for 1 or
6 days, or treatment with different sources of nitrogen
and carbon for 4 or 24 hours. CNA was prepared from 5 Ncg
of poly A+ selected RNA and was directionally ligated into
the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
/organism="Gallus gallus"
/mol_type="genomic DNA"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vitrogen) for propagation"
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/mol_type="mRNA"
/db_xref="taxon:3695"
/clone="GQ0123_E15"
                                                           1. .378
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31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             Magrini, V.,
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                                                                                                                                                           Conservative
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140 AGTAGTGCTATTTTAATTAAGTTAAGTTTAAGTTTTAGTTTTACTGTTCAGGATGCCTATTG 199
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO153155 433 bp mRNA linear LSI VERNO1401.5prime Exelixis FlyTag MNO8 BlueScript Drosophila melanogaster cDNA clone EN01401 5, mRNA sequence.
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EN.14 row: A column: 1
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CO153155
CO153155.1 GI:48907156
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exelixis FlyTag EST Project MN08 Library Unpublished (2004)
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Nakanishi,M., Muzong,C., Peterson,E., Laufer,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
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GCAGCCCCATAATATCCAGGACACCCTCTCTGCTTCTTATATGATTAG
                                                                                                ecennecros ana receive de la constanta de la c
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/clone_lib="Exelvise FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site 1: Not1; Site
/note="Vector: pBluescript; Site 1: Not1; Site
oligodT primed from LPS induced mbn2 cell line.
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/sex="female"
/clone_lib="Ggal_PR-1"
/note="produced by Cot-based cloning and sequencing (CBCS)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EN01401"
                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%; Score 36; DB 7; Length 433
37.0%; Pred. No. 35;
vative 23; Mismatches 45; Indels
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Pred. No. 27;
27; Mismatches
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JOURNAL COMMENT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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CO153765
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KEYWORDS
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CO153454
                                                                                                   REFERENCE
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Best Local S
Matches 40
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                                          TITLE
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and Swimmer,C.
Exelixis FlyTag EST Project MN08 Library
Unpublished (2004)
Contact: Stapleton, M.
                                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.

[ (bases 1 to 490)
                                                                                                                                                                                                                                         CO153765 490 bp mRNA linear EST 0: EN02756.5prime Exelixis FlyTag MN08 BlueScript Drosophila melanogaster cDNA clone EN02756 5, mRNA sequence.
CO153765 CO153765.1 GI:48907766
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Fax: 510 486 6798
Email: http://www.fruitfly.org/EST,
Plate: EN 20 row: A column: 10
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 486)
1 (bases 1 to 486)
Nakanishi, Muzong, C., Peterson, E., Laufer, A., Leung, W., Platt, D.
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Exelixis FlyTag EST Project MN08 Library
Unpublished (2004)
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One Cyclotron Rd, Berkeley, CA 94720,
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/note="Vector: pBluescript; Site_1: NotI; Site_
oligodT primed from LPS induced mbn2 cell line.
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/db_xref="taxon:7227"
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CO337794
LOCUS
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JOURNAL
Best Local Similarity Matches 40; Conserv
                                       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EN.153 row: B column: 5
                                                                                                                                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 539)
Nakanishi,M., Muzong,C., Peterson,E., Laufer,A.,
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swimmer, C.
  Conservative
                                                                                                                                                                                                                                                                             quality sequence stop: 474.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                              /clone lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site_1: NotI; Site_2: XhoI;
oligodT primed from LPS induced mbn2 cell line."
                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EN15317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site_1: NotI; Site_2:
oligodT primed from LPS induced mbn2 cell line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EN02756"
                                                                                                                                                          /cell_line="mbn2"
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/mol_type="mRNA"
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                  19.3%; Score 36; DB 37.0%; Pred. No. 36;
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                                     7; Length 539;
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45;
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era; Muscomorpl
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omorpha;
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RESULT 15
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BZ344795
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VERSION
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Best Local S
Matches 41
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                               275
                                                                                                                                                                                               215 GGTATGTTTAAAACTACTCTAATTTTTATAAATCATTTTTTAAAACTAGGTGCTTCCAA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
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                                                                                                                                                                                                                                             11 GAUCUGAUUAGAAGUAAGAAAUUCCUAGUUAUAUAUAUUUUUAAUACUGCUACAUUUUUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                       71 AGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCC 129
                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mccombie@cshl.org
Plate: hq90 row: h column:
Seq primer: -21M13UnivFwd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A. Zenawern, B., Sequences from Sorghum bicolor (methyl-filtere-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZ344795
638 bp DNA linear GSS 12-NOV-2002 hq90h10.b1 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum bicolor genomic clone hq90h10 5', genomic survey sequence.
  BH876088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum bicolor (sorghum)
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                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                           AGGCCCTAAGTTGCCAATATATATATACACCCGTCTTGGGTCCAGCAACTCAGCATCATGC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGCCCCATAATATCCAGGACACCCTCTCTCTCTTATATGATTAG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 638.
Location/Qualifiers
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  /clone libe-"MGS-Spicolorf (JM107 adapted methyl filtered) "
/note="Site 1: Xba I; Site 2: Xba I; The vector was
digested with XbaI and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (.x/y reads in M13mp19,
.b/g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="hq90h10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lab_host="JM107 or DH5a"
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; Pred. No. 42;
26; Mismatches
  666
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  DNA
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KEYWORDS
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                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                               Local
283 AGGCCCTAAGTTGCCAATATATATACACCCGTCTTGGGTCCAGCAACTCAGCATCATGC 341
                                                                                                   223 GGTATGTTTÄAÄÄÄCTÄCTCTÄÄTTTTTÄTÄÄÄTCÄTTTTTTTÄÄÄÄÄCTÄGGTGCTTCCAÄ 282
                                               71 AGACCCUUAGUUAUUVAGCUUVACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCC 129
                                                                                                                                     11 GAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUA 70
                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 666)

Rabinowicz, P. D., O'Shaughnessy, A. L., Balija, V., Dedhia, N. Katzenburger, F., King, L., Miller, B., Muller, S., Nasciment, Zutavern, T., McCombie, W. R. and Marrienssen, R. A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hr28h10.b1 WGS-ZmaysF (JM107 adapted methyl filtered) genomic clone hr28h10 5', genomic survey sequence. BH876088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mccombie@cshl.org
Plate: hr28 row: h column:
Seq primer: -21M13UnivFwd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH876088.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 666.
Location/Qualifiers
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                        /clone lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol_type="genomic D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:4577"
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                                                                                                                                                                                                                       19.1%;
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                                                                                                                                                                                                    26;
                                                                                                                                                                                                  Score 35.8; D)
Pred. No. 42;
26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dedhia, N.,
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2: /cgn2_6/ptcodats/l/ina/5_COMB.seq:*

3: /cgn2_6/ptcodats/l/ina/6A_COMB.seq:*

4: /cgn2_6/ptcodata/l/ina/6B_COMB.seq:*

5: /cgn2_6/ptcodata/l/ina/PTCTUS_COMB.seq:*

6: /cgn2_6/ptcodata/l/ina/PT_COMB.seq:*

7: /cgn2_6/ptcodata/l/ina/RE_COMB.seq:*

9: /cgn2_6/ptcodata/l/ina/RE_COMB.seq:*
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e 1697, Ap
e 1097, Ap
e 10221, Ap
e 14644, A
e 16464, A
e 1678, Ap
e 27423, A
e 27424, A
e 27424, A
e 27424, A
e 27424, A
e 12232, A
e 1232, A
e 1375, App
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25 31.4 16.8 96074 3 US-09-949-016-13611 Sequence 13611, A 16.8 110000 3 US-09-830-902-1 Sequence 13883, A 27 31.2 16.7 38705 3 US-09-949-016-13883 Sequence 13883, A 28 31.2 16.7 38705 3 US-09-949-016-13883 Sequence 13884, A 29 31.2 16.7 640681 3 US-09-949-016-1369 Sequence 13884, A 29 31.2 16.7 640681 3 US-09-949-016-13025 Sequence 13883, A 29 31.2 16.6 102053 3 US-09-949-016-13025 Sequence 13025, A 29 31 16.6 121970 3 US-09-949-016-13025 Sequence 13025, A 29 31 16.6 121970 3 US-09-949-016-13025 Sequence 13025, A 29 31 16.6 121970 3 US-09-949-016-15307 Sequence 13025, A 29 31 16.5 138282 3 US-09-949-016-15307 Sequence 13007, A 20 30 30 8 16.5 5935 3 US-09-419-568F-29 Sequence 17.216, Appli C 38 30.8 16.5 5935 3 US-09-419-568F-29 Sequence 29, Appli C 39 30.8 16.5 5935 3 US-09-319-568F-29 Sequence 29, Appli C 39 30.8 16.5 38702 3 US-09-349-016-13788 Sequence 29, Appli C 30 30.8 16.4 18620 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13788, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13781, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Sequence 13781, A 20 30.6 16.4 30327 3 US-09-949-016-13010 Se
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ALIGNMENTS

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US-09-270-767-16354
; Sequence 16354, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16354
LENGTH: 1345
TYPE: DNA
; ORGANISM: Drosophila melanogaster
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1072

LENGTH: 1345

TYPE: DNA

ORGANISM: Drosophila melanogaster
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Sequence 12956, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TORRENT FILL OR INVENTION: USBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12956

LENGTH: 18122
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US-09-543-681A-1097/c
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; LOCATION: (1) ... (18122)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-12956
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: 01/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1097
LENGTH: 861
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; Sequence 13291, Application US/09949016
; Patent No. 6812339
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US-09-949-016-1021
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                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: VENTER, J.
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1021
               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2000-04-14
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Local Similarity 34.5%; Pred. No. 1.7;
les 40; Conservative 24; Mismatches
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Gaps

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1768

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US-09-949-016-13563, Application US/09949016

Sequence 13563, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT APPLICATION UNIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
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US-09-949-016-16484
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; ORGANISM: Human
US-09-949-016-13291
                                                                                                                                                                                                                     RESULT 8
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Matches
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SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 16484
LENGTH: 26611
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SEQ ID NO 13291
LENGTH: 18008
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                   17732 TAGAGACAGAGTTTCGCTCTTGTCACCCAGGCTGGAGTGCAGTGGCCC 17779
                                                                                                                                                                                                                                                                                                                                                                    5998 AGACGGAGTCTTGCTCTGTCGCCCAGGCTGGAGTGCAGTG 5959
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                                                                                                                                                                                                                                                                                                                                                                                               72 GACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 32.8; DB 3; Length 26611; 32.4%; Pred. No. 4.2; ative 26; Mismatches 47; Indels 0;
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; ORGANISM: Human
US-09-949-016-13563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13563
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 20701:
                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 123
OTHER INFORMATION: y=c or t
                                              NAME/KEY: misc_feature
                                                                                         LOCATION: 130
OTHER INFORMATION: y=c
                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                      LOCATION: 127 TOTHER INFORMATION: 8=9
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: m=a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                LOCATION: 161 TOTHER INFORMATION: m=a or
                                                                           FEATURE:
                                                                                                                                                        FEATURE:
                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 127
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LOCATION: 122
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LOCATION: 95
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EATURE:
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;; Pred. No. 7.2;
21; Mismatches
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; NAME/KEY: misc_feature
; LOCATION: 183
; COTHER INFORMATION: w=a or
US-09-513-999C-9678
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US-09-949-016-27423
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Sequence 27424, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2077012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 27423
LENGTH: 601
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Best Local Similarity
Matches 35; Conserv
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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Best Local
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                               559 GTAAT 563
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37; Conserv
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27.1%;
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Pred. No. 1.4;
0; Mismatches 58;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 27424
LENGTH: 601
TYPE: DNA
CECANISM.
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US-09-949-016-69289
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US-09-949-016-27424
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 69289
LENGTH: 601
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                          121 GCAAU 125
                                                                                       499 TTCCTTATTATCTCTTTAATATACATAGGATCTGGGGGCCGGGTGCGGTGGCTCATGCCT
                                                                                                                                                                                  439 GTAAGTTTGTCTGTTTCATCTAAGTTTTCATATTTATTGATATAAAGATGTTCATACTAT 498
                                                                                                                                     61 UACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCU 120
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GTAAT 563
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29.6%; Pred. No. 1.4;
tive 30; Mismatches
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29.6%; Pred. No. 1.4;
tive 30; Mismatches
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FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PRILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEG ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 12232

LENGTH: 58593

TYPE: DNA

ORGANISM: Human
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; ORGANISM: Human
US-09-949-016-69290
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT TILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 69290
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
PEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1)...(58593)
OTHER INFORMATION: n = A,T,C or G
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OF DETECTION AND USES THEREOF
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Search completed: December 22,
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; ORGANISM: Human
US-09-949-016-13779
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US-09-949-016-13779
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-0-0-0
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                   Matches
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Patent No. 6812339
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 60593
                                                                       52412 GTAAT 52416
                                                                                                                                               52352 TICCTIATTATCTCTTTAATATACATAGGATCTGGGGGCCGGGTGCGGTGGCTCATGCCT 52411
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37; Conservative
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Pred. No. 9;
30; Mismatches
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Pred. No. 8.9;
30; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
               100.0 199
34.1 281
34.1 281
24.8 200
19.8 200
19.3 201
19.6 600
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18.6 600
18.5 18334
18.5 430442
18.5 18337
18.0 733
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18.3 370469
17.5 4992
17.5 4992
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Gapop 10.0 , Gapext 1.0
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187
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US-10-088-750B-2
US-10-088-750B-10
US-10-088-750B-4
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US-10-088-750B-3
US-10-088-750B-3
US-10-925-065A-267570
US-10-972-079-78753
US-10-972-079-78754
US-10-741-600-17646
US-10-741-7375-128
US-10-703-210-33
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Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 357570,
Sequence 78753, A
Sequence 17846, A
Sequence 128, Appl
Sequence 128, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 8321, Appl
Sequence 316834, A
Sequence 316834, A
Sequence 316834, A
Sequence 31794, A
Sequence 31794, Ap
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω u | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
| 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.8 |
| 17. | 17. | 17. | 17.3 | 17.3 | 17.3 | 17.3 | 17.2 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.4 | 17.5 |
| 1655 | 849 | 749 | 676 | 628 | 618 | 450 | 154 | 46951 | 26493 | 3660 | - | 731 | 724 | 601 | 744802 | 101046 | 101046 | 786 | 786 | 628 | 2714 |
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| US-10-106-698-662 | US-09-925-065A-89375 | US-09-925-065A-34307 | US-09-925-065A-684178 | US-09-925-065A-588924 | US-09-925-065A-419108 | US-09-864-761-6460 | US-09-864-761-23174 | US-10-091-281-2 | US-09-984-429-240 | US-11-097-143-37237 | US-11-097-143-27121 | US-09-764-891-2046 | US-09-925-065A-13092 | US-10-779-543-18995 | US-10-292-798-1369 | US-10-741-600-17753 | US-10-741-601-5689 | US-10-027-632-165261 | US-10-027-632-165261 | US-09-925-065A-588921 | US-10-342-887-1574 |
| | Seguence 89375, A | Sequence 34307, A | Sequence 684178, | Sequence 588924, | Sequence 419108, | Sequence 6460, Ap | Sequence 23174, A | Sequence 2, Appli | Sequence 240, App | Sequence 37237, A | Sequence 27121, A | Sequence 2046, Ap | Sequence 13092, A | Sequence 18995, A | Sequence 1369, Ap | Sequence 17753, A | Sequence 5689, Ap | Sequence 165261, | Sequence 165261, | Sequence 588921, | Sequence 1574, Ap |

ALIGNMENTS

US-10-088-750B-2

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Sequence 2, Application US/10088750B;
Publication No. US20040166486A1;
GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PP2001-016746
PRIOR APPLICATION NUMBER: PC7/JP01/00641
PRIOR APPLICATION NUMBER: PC7/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTMARE: PatentIn version 3.2
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Best Local S
Matches 187
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 199
TYPE: RNA
ORGANISM: Himetobi P Virus
181
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                                                                      GCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAU
UUCACUA 187
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                       100.0%; Score 187; DB 7; 100.0%; Pred. No. 8.9e-43; tive 0; Mismatches 0;
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RESULT

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PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 281
TYPE: RNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                   ; OTHER INFORMATION: The sequence is used only to illustrate secondary structures; OTHER INFORMATION: predicted by a computer program, MFOLD, as shown in Fig. 3. US-10-088-750B-10
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Query Match
Best Local Similarity
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Publication No. US20040166486A1
GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
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Best Local Similarity
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APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
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CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: UP P2001-016746
PRIOR FILING DATE: 2001-01-25
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TYPE: RNA
ORGANISM: Plautia Stali Intestine Virus
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34.1%;
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Score 63.8; DB 7;
Pred. No. 6.9e-08;
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Pred. No. 4.1e-08;
0; Mismatches 66;
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                                    Length 281
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Sequence 6. Application US/10088750B

Publication No. US20040166486A1

GENERAL INFORMATION:

APPLICANT: KANAMORI, Yasushi

TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation

TITLE OF INVENTION: Activity

FILE REFERENCE: 3190-015

CURRENT APPLICATION NUMBER: US/10/088,750B

CURRENT FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: JP P2001-016746

PRIOR APPLICATION NUMBER: DST/JP01/00641

PRIOR APPLICATION NUMBER: DST/JP01/00641

PRIOR FILING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 12
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US-10-088-750B-4
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24.8%; Score 46.4; DB 7;
Best Local Similarity 58.1%; Pred. No. 0.005;
Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10088750B Publication No. US20040166486A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4
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SOFTWARE: PatentIn version 3.2
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PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
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TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKASHIMA, Nobuhiko APPLICANT: KANAMORI, Yasushi
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TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 GCCCUCUCUGCGGUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GUGGACUUUAGGCUAAAGAAUUUUCACU 186
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US-10-088-7508-3
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; ORGANISM: Black Queen-Cell Virus
US-10-088-750B-6
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                                                                                                                              US-09-925-065A-267570
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SEQ ID NO 3
LENGTH: 201
TYPE: RNA
ORGANISM: Drosophila C Virus
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APPLICANT: NAKASHIMA, Nobuhiko APPLICANT: KANAMORI, Yasushi
                                                               Sequence 267570, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
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PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
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SEQ ID NO 6
LENGTH: 202
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                  AGUAGUGCUAUCUUAAUAAUUAAGUUAACUAUUUUAGUUUUAGUUUCAGGAUGCCUAUUG 113
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ilarity 53.5%;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 835698
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 267570
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Best Local
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Best Local
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum.
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR TILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCUACAUUUUUA 70
68 UUAAGACCCUUAGUUAUUUA 87
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; Pred. No. 8.5;
26; Mismatches
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Pred. No. 14;
25; Mismatches
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TTCCGACTCTAAGTACCTTA 89

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; TYPE: DNA
; ORGANISM: Chicken
US-10-972-079-78754
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; ORGANISM: Chicken 19866894368851_1
US-10-972-079-78753
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US-10-972-079-78753
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                                                          Query Match
Best Local :
                                                                                                                                                                                             SOFTWARE: PatentIN version 3.1 SEQ ID NO 78754
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                                                                                                                                                                                                                                CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF TITLE OF INVENTION: LIVESTOCK FILE REPERENCE: MMI1110-2
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISS, Sue K. APPLICANT: ROSENFELD, David APPLICANT: KERR, Richard
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BATES, Stephen
HOLM, Tom
AAUGUGUGAUUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCUAC
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35.5%; Pred. No. 14;
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                                                        Score 34.8;
Pred. No. 14;
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US-10-741-600-17646/c
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Publication No. US20040219528A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FRACEQ for Windows Version 4.0
SEQ ID NO 17646
LENGTH: 183334
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SEQ ID NO 128
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APPLICANT: CARGILL, Michele et al.
                                                                                                                                                              Matches
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APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CLOO1499
                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375
                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                        ENGTH: 430442
                                                                                                                                                                                   Local Similarity
                                                                             144777 ACTTTGTACATTTGTATTATAATAATAATAATAATTATTTTTGAGACAGAGTCTT 144718
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189795
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                                    73 ACCCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUU 117
                                                                                                                    13 UCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCUACAUUUUUAAG 72
                                                                                                                                                              29;
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Pred. No. 1.8e+02;
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RESULT 13

US-09-925-065A-708859/c

Sequence 708859, Application US/09925065A Publication No. US20050228172A9

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-88724
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-05-09
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-925-065A-88724
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; ORGANISM: Homo sapiens
US-09-925-065A-708859
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PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 88724, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
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  Query Match 18.2%;
Best Local Similarity 36.1%;
Matches 39; Conservative 2
                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 88724 LENGTH: 733
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Best Local
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.135
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; Score 34; DB 4; Length 733; pred. No. 26; 23; Mismatches 46; Indels
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Pred. No. 28;
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CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/326,532
PRIOR FILING DATE: 2001-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gelb, Bruce D.
APPLICANT: Tartaglia, Marco
TITLE OF INVENTION: NOOMAN SYNDROME GENE
FILE REFERENCE: 2420/1J059-US1
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 35
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(300000)
OTHER INFORMATION: where n may be a or
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                                                                  293886 CAGTGGTAC 293894
                                                                                                                                  293826 TTAATTCTGTTTAATTTTTAAAAAGTTCTTTTGTTTCACTCTGTCGCCCAGGCTGGAGTG 293885
                                                                                                 111 CAGCGUUCC 119
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Pred. No. 2.6e+02;
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata1/1/pubpna/US08_NEW_PUB.seq:*.

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3: /cgn2_6/ptodata1/1/pubpna/US07_NEW_PUB.seq:*.

4: /cgn2_6/ptodata1/1/pubpna/PCT_NEW_PUB.seq:*.

5: /cgn2_6/ptodata1/1/pubpna/US10_NEW_PUB.seq:*.

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569.190 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-95-561-13330

US-10-750-185-34828

US-11-121-086-6

US-11-121-086-6

US-11-155-492-1

US-10-995-561-13314

US-10-750-185-3690

US-10-750-185-3690

US-10-793-626-4256

US-11-17-995-561-52218

US-10-995-561-13421

US-10-995-561-13421

US-10-750-185-53040

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US-10-995-561-38114

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US-11-145-703-1

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Sequence 53, Appl Sequence 1330, A Sequence 1330, A Sequence 4, Appli Sequence 6, Appli Sequence 1314, A Sequence 36820, A Sequence 36820, A Sequence 42447, A Sequence 42, Appli Sequence 42, Appli Sequence 53218, A Sequence 53218, A Sequence 53040, A Sequence 50665, A Sequence 50665, A Sequence 5065, A Sequence 51314, A Sequence 53736, A Sequence 53736
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ü | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 7.3 |
| 28.8 | 28.8 | 28.8 | 28.8 | 28.8 | 28.8 | 28.8 | 28.8 | 29 | 29 | 29 | 29.2 | 29.2 | 29.2 | 29.2 | 29.4 | 29.4 | 29.4 | 29.4 | 9 | 29.6 | |
| 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.4 | 15.5 | 15.5 | 15.5 | ٠ و | 15.6 | 15.6 | 15.6 | 15.7 | 15.7 | 15.7 | 15.7 | 5 8 | 15.8 | |
| 1692 | 1459 | 1280 | 979 | 706 | 600 | 435 | 201 | 197096 | 110000 | 881 | 187745 | 7445 | 843 | 450 | 1125000 | 197781 | 137935 | 2261 | 1082144 | 398287 | - |
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| US-10-750-185-47673 | US-10-750-185-30881 | US-10-750-185-53636 | US-10-750-185-47956 | US-10-986-501-11 | US-10-750-185-21810 | US-11-194-246-475 | US-10-995-561-70950 | US-11-121-086-107 | US-11-155-492-1 | US-10-750-185-57774 | US-11-121-086-83 | US-11-177-987-8 | US-10-750-185-38003 | US-10-750-185-20090 | US-10-995-561-13286 | US-11-112-908-34 | US-10-995-561-13278 | US-10-750-185-58700 | US-11-117-187-211 | US-10-995-561-13396 | |
| Sequence 47673, A | Sequence 30881, A | Sequence 53636, A | Sequence 47956, A | Sequence 11, Appl | Sequence 21810, A | Sequence 475, App | Sequence 70950, A | Sequence 107, App | Sequence 1, Appli | Sequence 57774, A | Sequence 83, Appl | Sequence 8, Appli | Sequence 38003, A | Sequence 20090, A | Sequence 13286, I | Sequence 34, Appl | Sequence 13278, A | Sequence 58700, A | Sequence 211, App | Sequence 13396, A | -dd |

ALIGNMENTS

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RESULT 1

US-11-121-086-53/c

US-11-121-086-53/c

Sequence 53, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 99138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTIN VERSION 3.3

SEQ ID NO 53

LENGTH: 176503
                                                                                                                                                                          RESULT 2
US-10-750-185-54747/c
US-10-750-185-54747, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-121-086-53
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
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Best Local S
                                                                                                                                                                                                                                                                                                                                                 28041 TITGTITITAGCICIGITGCCCAGGCIGGAGIGCAGIGGCACAAICAIAGC 27990
                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 UUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AUUAGAAGUAAGAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUAAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 18.0%; Score 33.6; DB 7; Length 176503;
1 Similarity 26.8%; Pred. No. 4.4;
30; Conservative 33; Mismatches 49; Indels 0;
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RESULT 4
US-10-750-185-34828/c
US-10-750-185-34828, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(101046)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-095-561-13330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-995-561-13330/c
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US-10-750-185-54747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 54747
LENGTH: 1310
TYPE: Now
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: F885SEQ for Windows Version 4.0
SEQ ID NO 13330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13330, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION SUD USES THEREOF

FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
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CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 101046
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                                                                                                                                                                                                                   20925 TTATTTTGAGACGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGC 2087
                                                                                                                                                                             69 ИЛЛЕССИИЛЕНИАНИИЛЕСИИИЛЕССЕССАВВЛИВЕВИВСАВСЕНИЕС 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 AAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUUAAGACCCUUAGUUAUUUAG
                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                  l Similarity
36; Conserv
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                                                                                                                                                                                                                                                           GUGAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATATCACATTTATAATATTGGTAATACTAAAATAATATAGAAATACCTTAAATGTTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGGGCACCUAGGUGCAGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTAGTCTTAATACTGGTTTTGCTAGAAAA 462
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                                                                                                                                                                                                                                                                                                  17.4%; Score 32.6; Dilarity 32.4%; Pred. No. 7.1; Conservative 26; Mismatches
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; Pred. No. 1.1;
35; Mismatches
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US-11-121-086-4/c
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                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/11121086 Publication No. US20050266459A1
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 99138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

CURRENT FILING DATE: 2005-05-04
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIN version 3.1 SEQ ID NO 34828
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/567,570 PRIOR FILING DATE: 2004-05-04 NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE; MUILIOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2005-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                           TYPE: DNA
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ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                LENGTH: 164810
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                                                                                                                                                                                      Local Similarity
                                                                                  34668
34608 AMAATTGTCTCGCTGTGTTGCCCAGGCTGGAGTGTAGTG 34570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 АUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCUACAUUUUUUAAGACCC 76
                                  UUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCG 115
                                                                                АUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCUACAUUUUUAAGACCC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cuaeguecaeccuuguaeuuuuaeueeaecuaaaeaauuucaeu 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGGGTTTTTACCATTTCCTCTGAGATATTATGGCAGTATTCCACAAATAGCTATCCCAC
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                                                                                                                                                                   Conservative
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                                                                                                                                                                 17.0%; Score 31.8; D
36.4%; Pred. No. 15;
ative 21; Mismatches
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                                                                                                                                                                                                        Length 164810;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-6
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                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: R-341894
CURRENT APPLICATION NUMBER: US/11/155,492
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: US/09/830,902
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: FR 99 11097
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/FR00/02433
PRIOR APPLICATION NUMBER: PCT/FR00/02433
PRIOR FILING DATE: 2000-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/11155492
Publication No. US20050266479A1
GENERAL INFORMATION:
APPLICANT: Weissenbach, Jean
APPLICANT: Hazan, Jamil
TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPG4
TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 1
LENGTH: 110000
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION:
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Best Local (
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APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 99138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PELICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
                                                                                       FEATURE:
NAME/KEY: exon
LOCATION: (33719)...(33805)
                                                                                                                                           FEATURE:
NAME/KEY: intron
LOCATION: (10472)...(33718)
                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                               JAME/KEY: intron
JOCATION: (33806)...(35748)
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(35749)...(35832)
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(83335)..
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(82865)...(83102)
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(60864)...
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(45023)...(45118)
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(88130)...
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(82789)...(82864)
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(74634)...(74705)
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(73174)...(73248)
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(62345)...(62438)
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(89642)...(91162)
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(89562)...(89641)
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(88173)...(89561)
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(83103)...(83194)
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(73249)...(74633)
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CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13314

LENGTH: 119036

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(119036)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-01995-561-13314
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US-10-995-561-13314
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          Sequence 36820, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KOSENFELD, David
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Best Local S
Matches 31
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Best Local (
APPLICANT: APPLICANT:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
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LOCATION: (91234)...(93443)
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                                                        RESULT 11
US-10-793-626-4256
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APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 42447
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US-10-750-185-42447
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 36820
LENGTH: 879
CYPET-INS
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Best Local Similarity
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Publication No. US20050260603A1
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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                                                                                 28;
                                       61 UACAUUUUUAAGACCCUUAGUUAUUUA 87
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TTAÁTTATTTÁCÁATAATTGTTTATAÁ 711
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KERR, Richard
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ilarity 32.2%; Pred. No. 3;
Conservative 24; Mismatche
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                                                                                                                                                                    24; Mismatches
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Sequence 4256, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION:

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FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOPTWARE: PALENTIN Ver. 2.1
SEQ ID NO 4256
LENGTH: 4244
RESULT 13
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PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US/9/419,568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US/9/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US/9/178,973
PRIOR APPLICATION NUMBER: US/9/178,973
PRIOR APPLICATION NUMBER: US/9/178,973
PRIOR FILING DATE: 1998-10-26
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US-11-177-987-42/c
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 42
LENGTH: 5935
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Best Local (
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CURRENT FILING DATE: 2005-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: Interleukin-21, The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                           5862 TGTTGATATTAAAGGGAGAAAATTACAAGACAGAAGATTTATGATATTCATGTGTTTAT 5803
                                                                   5802 TAAAGCCTAAGATATCTTGTTT 5781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1231 TAAAAAAAAAGAGCT 1244
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                                                                                                                                                                                                    10 идаисиданиадаадиаадаааанииссиадинанананиининаниасидсиасанинин 69
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32.9%; Pred. No. 7.5;
ative 23; Mismatches
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Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                             DB 7; Length 5935;
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APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HERRY
APPLICANT: RENELAND, RIKARD HERRY
APPLICANT: REVEALIND, RIKARD HERRY
ITILE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
ITILE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
ITILE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
ITILE OF INVENTION: MUMBER: US/10/857,780
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILLING DATE: 2003-07-24
PRIOR FILLING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: Patentin version 3.2
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53218
LENGTH: 201
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROTH, RICHARD B
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEPJ
APPLICANT: NELSON, MATTHES
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 110950
                                                                                                102820 GTTCTGTGAAGAGAAAAAAATGTTGATTATTATTGATATTATCACATCATTTTTC 102879
102880 AGCCTCAAAGTAATTTA 102896
                                                                                                                                                                                                                        Local
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                                                71 AGACCCUUAGUUAUUUA 87
                                                                                                                                              11 GAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUA 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 UCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUUAAUACUGCUACAUUUUUAAAG 72
                                                                                                                                                                                            h 16.4%; Score 30.6; Similarity 36.4%; Pred. No. 31; 28; Conservative 20; Mismatches
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US-10-995-561-13421

US-10-995-561-13421

Sequence 13421, Application US/10995561

Publication No. US20050272054A1

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARCILL, Michele et al.
FITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF

FILLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION UNUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 13421

LENGTH: 403278

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: (1):..(403278)

COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13421
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Search completed: December 22, 2005, 16:41:00 Job time : 174.639 secs
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                                                                                                                        194981 CTCAGATTCTTGGGATTAAAATTCAAGCAGGGATGCAGTCTTCTTTTGAGTTACATG 195037
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                                                                                                                                                              76 CUUAGUUAUUUAGCCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGG 132
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         Best Local Similarity
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| Query Mat | FEATURES BOUTCE | JOURNAL | ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE | RESULT 1 BD173513 LOCUS DEFINITION | 0 0 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 37 6 5 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | la la |
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| ch 100.0%; Score 189; DB 6; Length 189; Similarity 64.0%; Pred. No. 2.3e-35; | PF 31-JAN-2001 W0 2001JP000641 PR 25-JAN-2001 JP 01P 016746 PI (NOBUHIKO NAKASHIMA,YASUSHI KANAMORI PC C12N15/11,C12N15/86,C12P21/02 PC CLOUNTS/11,C12N15/86,C12P21/02 PC CLOUNTS/11,C12N15/86,C12P21/02 PT Examslation activity PH Key Location/Qualifiers PT SOURCE /organism='Drosophila C virus'. PEATURES PT Location/Qualifiers 1. 189 90urce /organism='Drosophila C virus' //ob_ttype="genomic RNA" //ob_xref="taxon:64279" | PATENT: WO 02061080-A 3 08-AUG-2002; JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI OS DYOSOPHILA C VÍTUS PN WO 02061080-A/3 PD 08-AUG-2002 | activity. BD173513.1 GI:28414844 WO 02061080-A/3. Drosophila C virus Drosophila C virus Drosophila C virus Drosophila C virus Dicistroviridae; Cripavirus. 1 (bases 1 to 189) Nakashima, N. and Kanamori, Y. Novel tertiary structure having ability to accelerate translation activity | ALIGNMENTS BD173513 189 bp RNA linear PAT 18-FEB-2003 NOvel tertiary structure having ability to accelerate translation | 19.7 186045 S AL935182 19.7 233137 14 AC127758 19.6 218951 14 AC125915 19.5 110000 14 AC107134 2 19.5 128674 14 AC098368 19.5 147586 14 CR735143 19.5 180401 8 AC007489 19.5 212537 14 AC109658 | 99.6 21.0 52149 14 AC012958 AC012958 Drosophil 19.6 21.0 185200 2 AC092401 AC012958 Drosophil 19.6 21.0 191558 2 AC013431 AC013431 Drosophil 19.6 21.0 303344 2 AB003500 AE003500 Drosophil 19.6 2.0 3 108176 9 AL845327 AD0186 DNA 18.2 20.2 199631 8 AC146534 AC134709 AF178440 Triatrom 18.2 20.2 139631 8 AC146534 AC039247 ARTHUS no 19.8 20.1 234660 14 AC139709 AC134709 Rattus no 19.6 19.9 98121 13 AF336531 AP014 1et 19.6 19.9 98121 13 AF336531 AF336531 AP014 1et 19.6 19.9 10000 1 AE007332 6 AX763949 Sequence 19.7 19.8 174520 8 AC093432 AC093432 Homo sapi 19.4 19.8 174520 8 AC093432 AC139669 Bos tauru 19.5 227069 4 AC119141 AC119141 Rattus no | 21.1 181150 8 AC007256 21.0 5059 6 CO597290 |

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Dicistroviridae; Cripavirus.

CE 1 (bases 1 to 189)

RS Nakashima, N. and Kanamori, Y.

Novel translational activity-promoting higher-order structure patent: JP 2002306168-A 3 22-OCT-2002;

BIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES

OS Drosophila C virus
PN JP 2002306168-A/3
PD 22-OCT-2002
PF 25-TAN-2001 JP 2001016746
PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
PC C12N15/09.012N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02// PC
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C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02// PC
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Location/Qualifiers
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/mol_type="genomic RNA"
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181 AAATAACCT 189
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The novel genome organization of the insect picorna-like virus Drosophila C virus suggests this virus belongs to a previously undescribed virus family
J. Gen. Virol. 79 (Pt 1), 191-203 (1998)
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Drosophila C virus
Viruses; ssRNA positive-strand viruses,
Dicistroviridae; Cripavirus.
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Johnson, K.N. and Christian, P.D.
Direct Submission
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Drosophila C virus strain
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AF014388.1 GI:2388672
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VGQSGDVKTNKAQIKVEAGALELUTVALTGGGSDBAHNLLALDVPQKNTYRMSYFRG
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DKRYQLGNCTEVRGWSSFIMPYHFQAAVFARLLPNTIISLSQOMSEDLMGIPLSHFFS
AGVDMFYLTDNCVRLFFKNGIBFRDCVMVNLHSRMCTFHRDLVRHFILTSDQGKLKGGS
AGVDMFYLTDNCVRLFFKNGIBFRDCVMVNLHSRMCTFHRDLVRHFILTSDQGKLKGGS
GGAMATFHVNNMGLYRVYNMLNAVRPCDKKIEIFHFSDGFFYFSSYIQRDCVFYNAP
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TSNYALLKPTILANKVHNPLLSGKISNVIFTDFLKDERRDIAKVNVGKTRVFSAGPQHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGUGKTEMVYPLCIDVLREMGMIKKDDPHHQVYGRQVETEFWDGYKGQKIVIYDDAFQ
KXDDKTAANPEIFEVIRSCUT'E PQHLHMALHBKUT'ESAELLLYTTNDYNVKLESIT
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DRMDICLSDCKTYLAKKYEEIKKILAEHPILTILGMIGVALSALAMYYWFSKSLDVYE
DRMDICLSDCKTYLAKKYEEIKKILAEHPILTILGMIGVALSALAMYYWFSKSLDVYE
DRMDICLSDCKTYLAKKYEEIKKILAEHPILTILGMIGVALSALAMYYWFSKSLDVYE
DRMDICLSDCKTYLAKKYEEIKKILAEHPILTILGMIGVALSALAMYYWFSKSLDVYE
DRMDICLSDCKTYLAKKYEEIKKILAEHPILTILGMIGVALSALAMYYWFSKSLDVYE
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LQRHVAPLKIEVIYEMLNWSRRSIDPDEILMSNIETAFREVVYHGKEEYDKLRSAVLA
                                                                                                                                                                                VVAFRQYFLPFAAMLMHNRISNEVAVGTNVYSSDWERIAKRLKTKGSHVIAGDFGNFD
GSLVAQILWAIFWEIFVVWLKQFIDIENSEGKRILCICLGLWSHLVHSVHIYEDNVYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWFHTCGKIIFAVMAFLTIKKIPGKQDWDSYITRLDRIPKSIEGAKKITDYCSEYFNIANDQIKMMVLGKTKEELQRANGLYGEIQAWAQEVRQYLELDQRNKIDLDTETANRVEQLMIKGLKFKSEPLLSKEMSALVHTTLLPAKQLYEYVSCSPVKGGGPRMRPICLWLVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVYYRYNDPRYTRLEKAIERRDDKIKTLIKELRRQIKNRKIYSQGMFDKLTKQISDGI
KDGVGSEQMNGNLTRICDFLENTLPGLQANIQATVIDTTDKYVSLKEDIMKIVLVILL
VRLLMVMKKYRASLGVILIFIFKFYGFDQKLIDLIMDLKNKIFSQGALEDTVEEVVYH
                                                              LKVPQELPENPQILTYNQYLHDIEYLADPLYDF"
                                                                                                                                                      WTHSQPSGNPFTVIINCLYNSIIMRLSWIRVMEKFQPRLKSMKWFNEYVALITYGDDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC58807
/db_xref="GI:2388673"
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/mol_type="genomic RNA"
/strain="EB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="includes putative protease, helicase and lomains; putative; ORF-1"
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in EB, complete genome.
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codon_start=1

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ACCESSION
VERSION
KEYWORDS
SOURCE
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AR496112
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Best Local S
Matches 120
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Patent: US 6703491-A 1072 09-MAR-2004;
Exelixis, Inc.; South San Francisco, C
Location/Qualifiers
1. .1345
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Sequence 1072 from patent US 6703491.
AR496112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.
1 (bases 1 to 1345)
1 (bases 1 to 1345)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L.,
Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
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                                                                                                                                                                                                 Similarity
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AAATAACCT 6266
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                                                                                                                                                       99.2%; Score 187.4; DB 6
llarity 63.5%; Pred. No. 3.9e-35;
Conservative 68; Mismatches 1
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/protein_id="capid polyprotein"
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pridliblygryptganiftgssphfasigokysgdkftekdlkdiwtskaynkopd
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kifaynaseirolkescitseokeynseksiynkkiptikalsaoneietksgisgtspem
kifaynaseirolkescitseokeynseksiynkiptierksgisgtspem
kifaynaseirolkescitseokenseksiptikkiptsgislerrchardssilkonyvtenkikptsgisgtspem
dlshvlsiphfwdrftyffhgatsilkonyvtenkikptsgislorerchardsvorg
blshvlsiptiptyksrpwhyciffhgatatspertyknitsgirgvpurstokvivdlarnvegs
idtivevsggpdltfarenyphfassilkonalmynaspeahcigekimsir
glikevsggpdltptpahphapsyvpysggftladbaakkorespeahcigekimsir
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                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
/mol_type="genomic DNA"
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REFERENCE
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                               RESULT 6
BD173514
LOCUS
DEFINITION
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ORGANISM
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AR511394
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                  120;
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                                                  Cricket paralysis virus
Cricket paralysis virus
Viruses; serna positive-strand
                                                                                    activity.
BD173514
BD173514.1 GI:28414845
WO 02061080-A/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1345)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis
Homburger, S.A., Ebens, A.J. Jr., Ruddy, D.A. and Buchman, A.R.
Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
Drosophila sequences
Patent: US 6703491-A 16354 09-MAR-2004;
Exelixis, Inc., South San Francisco, CA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16354 from patent US AR511394
                  1 (bases 1 to 188)
Nakashima, N. and Kanamori, Y.
                                                                                                                                  Novel
                                                                                                                                           BD173514
activity
         Novel tertiary structure having
                                         Dicistroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                               tertiary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
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                                       Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                 68; Mismatches
                                                                                                                               188 bp
having
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S 6703491.
                                                     viruses,
                                                                                                                                 RNA
         ability
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          accelerate translation
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accelerate
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                                                                                                                                              PAT 18-FEB-2003
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RESULT 7
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JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENYONOLOGICAL SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI PN WO 02061080-A/4
PD 08-AUG-2002
PF 31-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 UP 01P 01674--
PI NOBUHIKO NAKASHIMA "
CC NOVP1
                                                                                                                                                                                   TITLE
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OS CITICKEt paralysis virus

ON JP 2002306168-A/4

PD 20-CT-2002

PD 22-CCT-2002

PP 25-JAN-2001 JP 2001016746

PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12R21/02// PC

(C12N15/09,C12N1/15,C12N1/19,C12N15/00,C12R1:92) CC

(NOVEL translational activity-promoting higher-order structure PH

Key GOLICE

LOCATION/Qualifiers
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/mol_type="genomic RNA"
/db_xref="taxon:12136"
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Pred. No. 1.4
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AP218039.1 GI:8895506
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Submitted (20-DEC-1999) Microbiology & Immunology, University, 299 Campus Drive, Stanford, CA 94305, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 9185)
Wilson,J.E., Powell,M.J., Hoover,S.E. and Sarnow,P.
Naturally occurring dicistronic cricket paralysis v
regulated by two internal ribosome entry sites
Mol. Cell. Biol. 20 (14), 4990-4999 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University, 299 Campus Drive,
Location/Qualifiers
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sernA positive-strand viruses,
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db_xref="taxon:12136"
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/mol_type="genomic RNA"
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Pred. No. 1.4e-19;
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AFOLKODKTIKUNDEI FEVIRTONTFOHILHMAALODKMYSOAEVLLYTINGFOYOLE SITFPDAFYNRHKTIA YRVQI KOEKSIRVRHARGEEYNALDVTKLNKLDAAI DLSVVE OKMREDDESATKMI DDESPISYDEFARTI CKAMKEEKEKTFHOLOMLEAY ASRTVAOG GSETSEYYDVMDETYFSNLLSQGFMAGKSLIEMEAEFASDAETFNAYIEYKKNIFKET ٦.

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RESULT 9
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Novel tertiary structure
activity.
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BD173516
BD173516.1 GI:28414847
WO 02061080-A/6.
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VVPYSHFIA PNAERVELITACTRIHYKDETPRDCYLVILHRMCHPHRDILKHFVKKS
DQGNLRGVFQGTLATFHQSANELCRAYQMLQAIRPLOQEITIYHEDTDMFDYESESYT
QRDCYEYNAFYQTGNGSIVGLYNKRWERKLIGMHIPGNYSECHGYACPLTQSESSYT
QRDCYEYNAFTQTGNGSIVGLYNKRWERKLIGMHIPGNYSECHGYACPLTQSESSYT
QRDCYEYNAFTQTSGNGSIVGLYNKGWERKLIGMHIPGNYSECHGYACPLTQSESSYT
QVBLTGYNNSLDVNKYRRFILTREATGTTGDFMKGIAKCGVDTAVLDAEIVESAALDVK
SCIYGMLSKFITKPAHLTRTRLPUGEIUDDFMKGIARQTSPGYRYFQMPRKLPGK
QVVLTQYNSMLDVNKYRRFLTYEEATGGTGDDFMKGIARQTSPGYRYFQMPRKLPGK
QDMMCSGEGYDFTSGRAQELRRDVEELLDNCAKGIIKDVVFUDTLKDERRFIEKVDAG
KTRVFSAGPQHFVVAPRKYFLPFAAYLMNNRIDNEIAVGTNYSTDWERIAKRLKCHG
NKYIAGDFGRYDAPRKYFLPFAAYLMNRIDNEIAVGTNYSTDWERIAKRLKCHG
NKYIAGDFGRYDAPRKYFLPFAAYLMNRIDNEIKTSDWKYETDGKKRALAPEMGSMKKFR
ENVSMISYGDDNCLNISDRVVEWFNQITISEQMKEIKHEYTDEGKTGDMVKFPSLSEI
HFLKKRFVFSHQLQRTAPLOKOVIYEMFNQITISEQMKEIKHEYTDEGKTGDMVKFPSLSEI
HFLKKRFVFSHQLQRTAPLOKOVIYEMFNQITISEQMKEITMMNITAFREIVYHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSTEVSPTVPYIASRPWLYCIRPESSWLSKDNKDGALMYNCVSGIVRVEVLNQLVAAQ
NVFSELDVICEVSGGPDLEFAGPTCPSYVPYAGDLTLADTRKLEABRTQEYSINNEDNR
ITTQCSRIVAQVMGEDQQIPNNEAQHGVHPISIDTHRISMSPQAMCIGEKIVSIRQ
LIKRFGIFGDANTLADAGSSFVVAAPFTVTSPTKTLTSTENYTQEDYXYLYAFWRGSM
RIKMVAETQDGTGTPRKKTNFTWFVRMFNSLQDSFNSLISTSSAVTTTVLPSGTINM
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product="strutral polyprotein"
protein_d="AAF80999.1"
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/translation="ATFODKQENSHIENEDKRLMSSSDPVEKCLYTANFPEVLISNA
VNLSTNYLDMTTREDKIHSIKDFLSGFIIIATMLMSSSDPVEKCLYTANFPEVLISNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKMVAETQDGTGTPKKKTNFTWFVRMFNSLQDSFNSLISTSSSAVTTTVLPSGTINM
GPSTQVIDPTVEGLIEVEVPYYNISHITPAVTIDDGTPSMEDYLKGHSPPCLLTFSPR
DSISATNHHITASFMKAPGDDFSFMYLLEVPPLVNVARA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKLFGFSKPTVQGKIGECKLRGQGRMANFDGMDMSHKMALSSTNEIETKEGLAGTSLD
EMDLSRVLSIPNYWDRFTWKTSDVTNTVLWDNYVSPFKVKPYSATITDRFRCTHMGYV
ANAFTYWRGSIVYTFKFVKTQYHSGRLRISFIPYYYNTTISTGTPDVSRTQKIVVDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYQDKLKGFYGLRATI LVKVQVNSQPFQQGRLMLQYI PYAQYMPNYTLI NETILQGRS
GCPTTDLELSYGTEVBRRI PYNSPHLYYNLI TGGGSFGSI YVVVYSQLHQQVSGTGSI
EYYWAAHLEDYDVQYETGANI FTGNSPSNYLSI JAERI AYGDFTETEMRKLMIHKYYLKR
PARI YAQAAKELKQLETNNSPSTALGQI SEGLTTLSHI PVLGNI FSTÞAWI SAKAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KWSKWMTILDEQISALSTKIRELKNKAYKFISEHPYLTALGFIGVMISAFAMYSFFER
TLTDDTITSEVGSSGDNKTQKISKRVVEVGGSGDVKTTKPAKTAVEVGSSGDSKTMKN
KITKVEVGSSGDSKTQKQRNTKVEVGKELEKEAETQGCSDPAAHALVLDVLQKNTYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEYQKLRSGIEDLAMKGILPQQPQILTFKAYLWDATMLADEVYDF"
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51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 123.6; DB 1
Pred. No. 6.5e-20;
                                                                                             190 bp
having
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                                                                                                RNA
ability to
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                                                                                                linear P.
accelerate
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ce translation
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BD177020
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ratent: WO 02061080-A 6 08-AUG-2002;
JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTONOLOGICAL SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

WMENT OS Black queen-cell virus
PN WO 02061080-A/6
PD 08-AUG-2002
PF 31-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 WO 2001JP000641
PR 25-JAN-2001 WO ANAKASHIMA
CC N-
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Best Local S
Matches 69
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Novel translational activ
BD177020
BD177020.1 GI:30014280
JP 2002306168-A/6.
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                                                                               INICLESSITED.

1 (bases 1 to 190)

1 (bases 1 to 190)

Nakashima, N. and Kanamori, Y.

Novel translational activity-promoting higher-order structure Novel translational activity-promoting higher-order structure Patent: JP 2002306168-A 6 22-OCT-2002;

PRESCTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMESTRY AND SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
FISHERIES
OS Black
PN JP 20
PD 22-00
PF 25-J#
                                                                                                                                                                                                                                                             unidentified
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                                                                                                                                                                                                                                          unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATATCTAGGAGAACTGTGCTATGTTTAGAAGATTAGGTAGTCTCTAAACAGAACAATTT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUAUCCAGGACACCCUCUCUGCUUCUVAUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAAU 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAU-UGGCAGCCCCAUA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUGUGAUCUUGCUUCCUUAUAC-AAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUC 65
                  JP 2002306168-A/6
22-OCT-2002
25-JAN-2001 JP 2001016746
                                                          Black queen-cell virus
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/mol_type="genomic RNA"
/db_xref="taxon:32644"
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37.7%; Pred. No. 1;
tive 41; Mismatches
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ORGANISM
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AF183905
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    Dicistroviridae; Cripavirus.

1 (bases 1 to 8550)
Leat,N., Ball,B., Govan,V. and Davison,S.
Analysis of the complete genome sequence of black queen-cell virus, a picorna-like virus of honey bees
J. Gen. Virol. 81 (Pt 8), 2111-2119 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
                                                                                                                                                                                                                                                                 Submitted (06-SEP-1999) Microbiology, University of Western Cape, Modderdam Rd., Cape Town, Western Cape 7535, South Africa
                                                                                                                                                                                                                                                                                                         2 (bases 1 to 8550)
Leat, N. and Davison, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black queen cell virus
Black queen cell virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Black queen cell virus
structural polyprotein
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PC C11815/09,C1281/15,C1281/19,C1281/21,C1285/10,C12921/02// PC
(C12815/09,C1281:92),C12815/00,(C1281:92) CC
(C12815/09,C1281:92),C12815/00,C1281:92) CC
Novel translational activity-promoting higher-order structure FH
Key Location/Qualifiers
FT 1.190
FT 1.190
FT /organism='Black queen-cell virus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF183905.1 GI:8100530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUGUGAUCUUGCUUCCUUAUAC-AAUUUUGAGAGGUUAAUAAGAAGGAAGGAGUGCUAUC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTGGAATCACCGTACCTATTTAGGTTTACGCTCCAAGATCGGTGGATAGCAGCCCTATC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTGATCTTGCTTGCGGAGGCAAAATTTGCACAGTATAAAATCTGCAAGTAGTAGTGCTATT 66
/codon_start=1
/product="nonstructural_polyprotein"
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/mol_type="genomic RNA"
/strain="South African"
/specific host="Apis mellifera"
/db_xref="taxon:92395"
                                                                                                                                                                                                                                                    Rd., Cape Town, West
Location/Qualifiers
                                                                    gene="orf1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
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37.7%;
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Pred. No. 1;
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gene Sas

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/genes"orf2"
5834. 8395
/gene="orf2"
/gene="orf2"
/note="capsid polyprotein; translation initiation most
likely facilitated by an internal ribosome entry site
(IRES); a region similar to Plautia stali intestine virus
IRES was identified immediately upstream of orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCFATPFYLEDVKEILSRYDYKAQSCAFELVLRODLEPCALPNHLDECEFILMGKVKD
PPVQPSRSKISPSPLYCHITEPSSAPTWLYPRELDGQIFDFLKYRTARLGKDSYPIRS
KLINLAKWALIDDIYSYYLQKKDLLDGRFPSSLTFPQAAVIF
GEDDYVNSIKRDTSCG
YPFVKEGWTRAKIFGNODSYDWSTSGYQMLREKVQECIEAARQGKILDHYFIDTLKDE
RKPKHKAHKSRMFSNGPIDYLVWSKMYFNPIVAVLSELKNVDHISVGSNVYSTDWDVI
RRYLKSKSHHWVAGDFEGFDASSQSDILYAAGEVLQELSKKIFNSTEDBMLQQRAIIH
SLVNSHINENGIVLGWCKSLPSGHYLTAIINSVFVNLWCLVFMEANQKYSFTTASS
FFRECGIVAYGDDHVVSVBEKKISVFNQCTLFVLMSKFGMFYTIETKDDTEIDFLSRR
IEDVSYLKRNFVYDESRQRYLAFLSLDVVLEMPMWTKSSKDIYTNVFCNLEHALKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRAYELDDGAILQFNHPYGKRNFFTFIGDIQFSLYKTKNISKTNDLDSRDLMHFVVDK
SVVHRDISSYFCERLELQSVGSTRIQLPVMRWVRDVGYIFVKSGQGTSCIKNVSNVSY
MTDTDPDAREIRLREAWEYSLETISGDCGAPLFVTNSKIGPGKIIGIHTAGGHRFGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OQLVTVIPDDROQOUDSSANPSLELFEIIRSSNIFPYPLHMASIEEKANTVFQSKVILC
SSNNKTPKTESLNYPKALLKREKAKVEKKRABESEGTTSTDCYTFVEYDFDHCNIVK
SMSFNELIDEVVAMYFHEGEFVSSUNFIMENVFAQGGGSLSDEEDDFIEASSYGDSL
LDEALTREEKKEIIECINDQFKNENDTRTSFQLIRDYFHCAKDSLQEKFLAYRRKYSF
DDWFSFSKASKVVLGILSLULVGYGIYSYVKGNPAKDSABSYERASKAKVEGSNGV
PEAYESKVNRKINVEGYARDLKKYGIYSYVKGNPAKDSABSVENGAKAKVEGSNGV
PEAYESKVNRKINVEGYARDLKKYGIYSYNTILSKESUIRVGHCIFLKGKIAVAPGHYLRIL
VQSBACSDINASEQLTAYTTNNTYNTTILSKESVIRVGHCIFLKGKIAVAPGHYLRIL
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DIKRLYNMGVSYMRHPLYKPHQRVISEILNQLLRFADKIKKKVGTDASVRNPPVTLYL
YGETGVGKSTLTYPLCATLLKTIFTREGNTVMLESLKQHYKGMIYVRAAEQEFWDGYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHDKELWEKWSPVLHSKSEEVLKMVSSLKFQDEVREIALGLSGYE"
codon_start=1
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ISRATKFFGASFSTISTVLITLITMTVTDKLVKKFLVDYYSKHMENAKMLAQAGEEDS
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FLKSGANWVSENILQPADĒIIGPILSLEGFSKPLLPITNPTVLRPANĪFAITDTNDMS
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KKGMYAQSNSGTEQQNPRGSSILTDEBSITKSDPYNPNISLLISGEVFTNFRNLIKRV
NFRKATTLNGKRISDITGINSLIEAPRLDIAQVVDTETKEAKYGFSYFMSAPTTLNIV
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밁 Matches Query Match Best Local 5653 99 69; Similarity UUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAU-UGGCAGCCCAUA 124 ATGTGATCTTGCTTGCGGAGGCAAAATTTGCACAGTATAAAATCTGCAAGTAGTGCTATT 5712 AUAUCCAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAAU 184 GTTGGAATCACCGTACCTATTTAGGTTTACGCTCCAAGATCGGTGGATAGCAGCCCTATC 5772 AUGUGAUCUUGCUUCCUUAUAC-AAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUC 65 Conservative 24.0%; 41; Score 45.4; DB 13; Pred. No. 0.48; 1; Mismatches 71; Indels Length 8550; 2; Gaps

(GTPPCIHASQTAQFTKIKQGKVYDLRYDQYDPFREVQDGTAFLNARSIEDSDLL"

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AF482758 224499
Cowpox virus strain Brighton
AF482758 J02066 L08906
AF482758.2 GI:30795158
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1. .1347
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Smith, C.A., Goodwin, R.G. and Pickup, D.J.
Cowpox virus Encodes a second soluble TNF receptor
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                                                                                                                                                                                                                                                                                                                    TCATCTTGTTTACAATTTATTTCCATAAGTATTTTATTATGACACACCGATTAATAT 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="soluble TNF receptor CrmC"
/product="soluble TNF receptor CrmC"
/protein_id="AAD10325.1"
/db_xref="GI:4097322"
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KVKCTGTQNSKCSCLPGWFCATDSSKTBDCRDCIPKRKCPCGYFGGIDELGNPLCKSC
CVGEYCDDIRNHRVGPFPPCKLSKCN"
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(strain="Brighton Redgene"
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3 (bases 1 to 224499)
Hu,F.Q. and Pickup,D.J.
Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution initiated from (2). 716-720 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 224499)
Pickup, D.J., Bastla, D., Stone, H.O. and Joklik, W.K.
Sequence of terminal regions of cowpox virus DNA:
repeated and unique sequence elements
Proc. Natl. Acad. Sci. U.S.A. 79 (23), 7112-7116 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pickup,D.J.
Direct Submission
Submitted (03-AUG-1993) Molecular Genetics and Microbiology,
Submitted (03-AUG-1993) Molecular Genetics and Microbiology,
University Medical Center, Box 3020 DUMC, 421 Jones Building,
Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 (bases 1 to 224499)
Hu,F.Q., Smith,C.A. and Pickup,D.J.
Cowpox virus contains two copies of an early gene soluble secreted form of the type II TNF receptor Virology 204 (1), 343-356 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-2003) Molecular Genetics and Microbiology, Duke University Medical Center, Box 3020 DUMC, 421 Jones Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-FEB-2002) Molecular Genetics and Microbiology, University Medical Center, Box 3020 DUMC, 421 Jones Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (bases 1 to 224499)
Dietrich, F.S., Ray, C.A., Sharma, D.A., Allen, A. and Pickup, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 175 (1), 69-80 (1990) 2309453
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Durham, NC 27710, USA
On May 16, 2003 this sequence version replaced gi:20152989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dietrich, F.S., Ray, C.A., Sharma, D.A., Allen, A. and Pickup, D.J. Direct Submission
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Durham, NC 27710, USA
7 (bases 1 to 224499)
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Parsons, B.L. and Pickup, D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 224499)
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complement(156. .350)
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                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .224499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7112-7116 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding
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Sdo
                                                                                          gene
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DNIDDFSKSSDLLLCYLRYKTNRLNYYVLYKLLTKGSDTNCVDEDGLTSLHYYCRHI
SFFHENNYYETKRYTKMYAEKRFINTIIDHGANINAVIGNTPLHTYLOBHTKHSPR
VVYALLSRGADTRIRNNFDCTPPIMEYIKNDCVACHILLLLLMMTEGKYOKLOKKYASYLVYI
SFFHENNYYETKKTSIDILRYLLDRFDIQKDEYYNTMTPLHAAFQNCNNKVASYLVYI
GYDINLFTKOGKTVFDLVFENNNLIYKSDVHHDIIRHLLKVSLDMIKSLFYRMSBEFSP
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RLKEIRISDTDLYTVLRTEDIRYHTYLEAIHSDKHISFPMYDDLIEQCHLSMKYKSKL
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Complement (4798. .6657)
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gene="CPXV007 CDS"
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WELELVISLCVSHLEGIWLSTSRTLPT"
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3482. .3697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKVTKQDQTPTNDKICQSVTEVTESEDESEEVVKGDPTTYYTVVGGGLIMDFGFTKCP
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SNIKTHPVLGSNISHKKVSYEDIIGSTIVDTKCVKNLEISVRIGDMCKESSELEVKDG
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complement(2743. .3483)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="soluble secreted TNF receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CPXV004 CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="vCCI"
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RESULT 14
AC109571
                   DEFINITION
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Best Local
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                                                                                                                                                                                 177424
                                                                                                                                                                                                                                                                                                                                                                                177544 TGAATATGATTCTTTATAAAATTTGAACAAGCTGAGTATAAGGATGTATTGTGTATTAAT 177485
                                                                                                                                                                                                                                                                            177484 TCATCTTGTTTACAATTTATTTCCATAAGTATTTTATATTATTAGGACACCGATTAATAT 177425
                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                                                                                     AC109571 334371 bp DNJ
Rattus norvegicus clone CH230-312G23,
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                                                                                                                                                                                                                          CAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAAUAAC 187
                                                                                                                                                                                                                                                                                                                               ИААППАGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUC 129
                                                                                                                                                                        CAAGAAATAAATAAGATAATTATTAATAGATCTTCATACTGAATAATACGCTACC 177367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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ETAGSLYRLLISYRTDATELFGSELKEFSDSLPWDNIDNCVGIINCFIRNESMKTAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (9013 . .9474)
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complement (9013 . .9474)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="CPXV010 CDS"
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GRHKELKRYRADINRMKNAYISGVSMFDILFKRNRRHRLRYAKNPTFINFVSNIKWYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.4%; Score 40.4; DB 13; 30.9%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.1;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               experimental
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DNA
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             linear HTG 08-OCT-2002
SEQUENCING IN PROGRESS
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ACCESSION

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REFERENCE
AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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Submitted (08-OCT-2002) Human Génome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21738310.
                                                                                                                                                                                                                                                       pirect Submission
Submitted (05-FRB-2002) Human Genome Sequencing Center, Department
Submitted (05-FRB-2002) Human Genetics, Baylor College of Medicine, One
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AC109571.4 GI:22856817
HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
                                                                                                                                                                                                      of Molecular and Human Genetics, Baylor Plaza, Houston, TX 77030, 3 (bases 1 to 334371)
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1 (bases 1 to 334371)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                       Rat Genome Sequencing Consortium
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FEATURES
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305611 TTCTCTTCTTTTAGGTTGAGTGTATCTGGTTTTA 305644
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                   305551 ATAAGCCATTGGTGTTCTGTTCAGGAAGTTTTCCCCCTGTGCCCATGTGTTCAAGGGCACT 305610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Institute of 334371; contig of 334371 bp in length.
                                                                                                                                                                                                         79 UAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUCCCAGGACACC 138
                                                                                                                                                                                                                                                                                                                                            19 UUCCUUAUACAAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUCUUAAUAAUUAGGU 78
                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequences only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                 CUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estimated insert size: 180965; sum-of-contigs estimation Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: phrap; version 0.990329
Assembly program: phrap; version 0.990329
Consensus quality: 165024 bases at least Q30
Consensus quality: 167701 bases at least Q30
Consensus quality: 169165 bases at least Q20
Consensus quality: 169165 bases at least Q20
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Center clone name: CH230-312G23
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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331962. .334371
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148486. .149650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Rattus norvegicus"
|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                              21.4%; Score 40.4; DI 29.2%; Pred. No. 3.8; tive 38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      71;
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| AC122491 AND MAIS MASC clone RP24-39DD3 from chromosome 3, complete sequence. AC122491.3 Gi:46559826 HTG. Blkarmecu Metazos; (Chordats; Craniara, Vertebrata; Enteleostomi; Metazos; (Chordats; Craniara, Vertebrata; Enteleostomi; Metazos; (Chordats; Craniara, Vertebrata; Enteleostomi; Metazos; (Chordats; Muridae; Murinae; Mus. Bukarmecu Metazos; (Chordats; Craniara, Vertebrata; Enteleostomi; Metazos; Conton, M., Bacilcki, L. and Meyer, R. Buyern, C., Cotton, M., Bacilcki, L. and Meyer, R. Brect Submission and Waterston, R. H. Direct Submission and Submission and Sequencing Center, 4444 Forest Park A (Labses 1 to 175092) MINON, R. K. Direct Submission and Sequencing Center, 4444 Forest Park A (Labses, Mo 63108, USA A (Labses, Mo 63108, | FEATURES | | | | | | COMMENT | | REFERENCE | TITLE JOURNAL | REFERENCE | TITLE JOURNAL | REFERENCE AUTHORS | Ž | AUTHORS | 22 | AUTHORS | REFERENCE | ORGANISM | VERSION KEYWORDS | DEFINITION | LOCUS |
|---|--------------------------|--|-----|---|---------|------------|---------|--------------------------------------|-----------|----------------------------|-----------|----------------------------|---|----------------------------|-----------------------------------|--|------------------------|---|----------|---------------------|-------------------------------|----------------------|
| | of the clone. This clone | SOURCE INFORMATION: The RPCI-24 BAC Library has been constructed by Pieter de Jong and Coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org | ₩ 6 | s sequence was finished as follows unless otherwise noted: regions were double stranded, sequenced with an alternate mistry, or covered by high quality data (i.e., phred quality; an attempt was made to resolve all sequencing problems, suc compressions and repeats; all regions were covered by at leas plasmid subclone, fosmid clone or direct clone walk sequence mence from the Mouse Genome Sequencing Consortium whole genom trum may have been used to obtain the consensus sequence; and assembly was confirmed by restriction digest. | NOTICE: | Sequencing | lence | enome Sequencing Center, 4444 Forest | , and | encing Center, 4444 Forest | , | encing Center, 4444 Forest | 3 (bases 1 to 175092) McPherson,J.D. and Waterston,R.H. | encing Center, 4444 Forest | McPherson,J.D. and Waterston,R.H. | Unpublished (2001) 2 (hases 1 to 175092) | otton, M., Bielicki, L | Ammalia; Eutheria; Emarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (hases 1 to 175092) | musculus | 22491.3 G | KF24-390D3 IFOM CHICMOBOME 3, | 175092 bp DNA linear |

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                                    166276 AACTAAAACATCTACTTTGTCTTTTGCTAATGCCCTTTATTATTATTCTTGTGGCCTCCAC 166217
                                                                                                                                 166336 TTAAGATTTGGACAGAATTCCTGAAAAGCATTTTAATAGAAATTGAGAGTGTAGCATTTC 166277
182 AAUA 185
||:|
                                                           122 АИААИАИССАССАССАСССИСИСИССИИСИИАИАИСАИИАССИИСИСТИИИАСААИИАСАА 181
                                                                                                      62 UAUCUUAAUAAUUAGGUUAACUAUUUAGGUUUACUGUUCAGGAUGCCUAUUGGCAGCCCC 121
                                                                                                                                                      /rpt_family="L1"
62968. .63143
/rpt_family="L1"
64971. .65431
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34234. .3
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                                                                                                                                                                                                                                                                                /note="Sequence derived from PCR product of project DNA."
62387. .62970
                                                                                                                                                                                                                                                                                                                                                                           /rpt_tamlly-.52714. .53646
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41958. .41994
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44352. .45342
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family="B4"
5. .43736
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6. .41652
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6. 40396
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3. .39160
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d. No. 18 the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

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| 18.4 | 18.5 | 18.5 | 19.0 | 19.0 | 19.3 | 19.3 | 19.9 | 20.8 | 21.0 | 21.1 | 21.1 | 21.1 | 24.0 | 24.0 | 65.4 | 65.4 | 100.0 | 100.0 | Query | عد ' |
| 37184 | 271990 | 271990 | 199 | 187 | 198 | 186 | 9829 | 460 | 5059 | 84476 | 45017 | 43938 | 202 | 190 | 200 | 188 | 201 | 189 | Query Match Length | |
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| ABQ67078 | ADN61228 | ADD25213 | AAL50545 | ABZ80708 | AAL50548 | ABZ80711 | AAL60324 | ACH45871 | ABL18538 | ADQ97028 | AAK77217 | AAK77216 | AAL50549 | ABZ80712 | AAL50547 | ABZ80710 | AAL50546 | ABZ80709 | ID | |
| Abq67078 Human ang | Adn61228 Radish nu | Add25213 Fertility | Aal50545 Himetobi | Abz80708 Himetobi | Aal50548 Triatoma | Abz80711 Triatoma | Aal60324 Aphid let | Ach45871 Human foe | Abl18538 Drosophil | | Aak77217 Human imm | Aak77216 Human imm | Aal50549 Black que | Abz80712 Black que | Aal50547 Cricket p | Abz80710 Cricket p | Aal50546 Drosophil | Abz80709 Drosophil | Description | |

The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

WPI; 2003-403230/38.

Nakashima N,

Shibuya N,

Nishikawa

s

(NAAG-) NAT INST AGROBIOLOGICAL SCI. (WAKE-) WAKENYAKU KK.

Claim 1; Page 32; 39pp; Japanese.

| | | | | | | | | | | | | | O | | | | | | | | | | | a | n |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 5 | 3 <u>4</u> | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
| 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.6 | 32.8 | 32.8 | 33 | 33 | υ U | 33.4 | 33.4 | 33.4 | 33.4 | 33.6 | 34 | 34 | 34 | 34.4 | 34.6 |
| 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.2 | 17.4 | 17.4 | 17.5 | 17:5 | 17.5 | 17.7 | 17.7 | 17.7 | 17.7 | 17.8 | 18.0 | 18.0 | 18.0 | 18.2 | 18.3 |
| 9760 | 9760 | 9760 | 9642 | 7355 | 6815 | 6815 | 6815 | 6815 | 6815 | 17389 | 6478 | 6478 | 208765 | 127432 | 18218 | 5544 | 5544 | 5544 | 5544 | 5273 | 12409 | 6815 | 6815 | 130263 | 4328 |
| σ | σ | თ | თ | σ | 10 | 10 | σ | 0 | 4 | σ | 13 | 10 | 12 | 12 | σ | 7 | σ | σ | σ | σ | σ | 10 | 5 | σ | N |
| AAS61156 | ABL70198 | ABK31243 | ABL32357 | ABN80297 | ADE84131 | ADB54195 | ABK28175 | ABL32670 | AAS45344 | ABL33415 | ADS89582 | ADB54284 | ADQ97430 | AD043653 | ABL33949 | ADS99881 | AAS61440 | ABL70477 | ABL34620 | ABL32875 | AAS63312 | ADE84207 | ADB54323 | ABK83573 | AAQ28758 |
| Aas61156 Human gen | Abl70198 Chemicall | Abk31243 Signal tr | Abl32357 Human imm | Abn80297 Human che | Ade84131 Human lym | Adb54195 Pretreate | Abk28175 DNA trans | Abl32670 Human imm | Aas45344 Chemicall | Abl33415 Human imm | Ads89582 Oligonucl | Adb54284 Pretreate | Adq97430 Mouse can | Ado43653 Nucleotid | Abl33949 Human imm | Ads99881 Bisulphit | Aas61440 Human gen | Abl70477 Chemicall | Abl34620 Human met | Abl32875 Human imm | Aas63312 Chemicall | Ade84207 Human lym | Adb54323 Pretreate | Abk83573 Human cDN | Aaq28758 Partial s |

ALIGNMENTS

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RESULT 1
ABZ80709
ID ABZ88
XX ABZ8
XX ABZ8
XX P8eu
DT 15-0
DT 17-0
DT WD20
XX WD20
XX WD20
XX WD20
XX WD20
XX WD20
DR WP1;
XX The
CC 11he
CC from
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                                                                                                                                                                                                                                                                                                                                                                                                  Pseudoknot; secondary structure; cell-free protein synthesis; wheatgerm; albumen; impurity; higher-order structure; intergenic region; IGR-IRES; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                              17-OCT-2001; 2001JP-00319923.
                                                                                                                                                                                                                                                                                                                                                                         Drosophila C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila C virus derived pseudoknot sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ80709 standard; RNA; 189 BP.
                                                                                                                                                                                                                                                                                        08-OCT-2002; 2002WO-JP010447.
                                                                                                                                                                                                                                                                                                                   24-APR-2003.
                                                                                                                                                                                                                                                                                                                                               WO2003033719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABZ80709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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RESULT 2
AAL50546
ID AAL5
XX AAL5
XX CrPN
CCPN
KW drug
KW prot
XX Drof
XX Drof
XX Drof
XX Drof
XX Drof
XX PD 08-j
XX (NA
XX NA
PA (NA
XX WPI
PT Tra
PT Tra
PT Syn
P
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Best Local
                         have a higher-order structure that sustains translational activity-
promoting function. The RNA sequences of the invention are useful in the
synthesis of proteins and polypeptides for application in developing are
producing drugs. The RNA sequences of the invention are also useful in
basic research of protein synthesis and structural analysis by the gene
                                                                                                                                                                                                                                                                                               Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;
                                                                                                                                                                   The invention comprises seven RNA sequences (CrPV-like viruses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2001; 2001JP-00016746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2001; 2001WO-JP000641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAAG-) NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila С
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                                                                                                                                                                                                                      Fig 1-2; 38pp; Japanese.
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Pred. No. 2.4e-43
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Best Local (
                                     The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Cricket paralysis virus. The "sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in
                                                                                                                                                                                                                                                                                                                               Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining transl activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                       Claim 1;
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Pred. No. 2.5e-43;
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                        Query Match
                                                                                                                                             The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Cricket
                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                             Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UAACCU 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAU 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ААЛАЛССАGGACACCCUCUCUGCUUCUJAJAJGAUJAGGUUGUCAUUJAGAAJAAGAAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UUUUUUGUAUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCAC 122
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                                                                          200 BP;
                                                                                                                             Virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kanamori
                                                                                                                             RNA
                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; higher-order structure; drug development;
translational activity-promoting function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGROBIOLOGICAL
                                                                        A; 36 C;
                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.4%;
65.4%;
79.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
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                                                                     37 G; 0 T; 67 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 123.6; DB 8
Pred. No. 5.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
Score 123.6; DB 6
Pred. No. 5.8e-25;
                                                                                                                             of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCI
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                        DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
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Best

Local Similarity

Query Match Best Local Similarity

24.0%; 60.1%;

Score 45.4; DB 8; Pred. No. 0.0054; 0; Mismatches 71;

71;

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Gaps

2

Length 190; Indels

Conservative

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190

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                                                                      from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Black queen-cell virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in
                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 34; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black queen-cell virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudoknot; secondary structure; cell-free albumen; impurity; higher-order structure; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Black queen-cell virus derived pseudoknot sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ80712;
                                                                                                                                                                                                                                                                               The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo
                                                                                                                                                                                                                                                                                                                                                                                                                          activity and function promotion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-403230/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2001; 2001JP-00319923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ80712 standard; RNA; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAAG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAT INST AGROBIOLOGICAL WAKENYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCUUAAUUAGUUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAU 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UAACCU 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAU 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAUAUCCAGGACACCCUCUCUGCUUGUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UUACCU 188
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  58
                                                        proteins
A; 36 C;
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  56 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein synthesis;
intergenic region;
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IGR-IRES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                             Matches 110;
                                                                                                 Query Match
                                                                                                                                                                       The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Black queencell virus RNA sequence of the invention. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                    Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2001; 2001WO-JP000641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-627482/67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Black queen cell virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200261080-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein synthesis; structural analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL50549 standard; RNA; 202 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NAAG-) NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2003
19-DEC-2002
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                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                        drugs.
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                                                                                 Similarity
 AUGUGAUCUUGCUUCCUUAUAC-AAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUC
                                                                                                                                   202 BP; 63 A; 38 C; 42 G; 0 T; 59 U; 0
                                                                                                                                                                                                                                                                                                                                                              Fig 1-2; 38pp; Japanese.
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(first entry)
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                                                                         24.0%;
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                                                           0;
                                                                             Score 45.4;
Pred. No. 0.
                                                         Mismatches
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                                               0.0055;
71;
                                                                                           DB 6;
                                                                                                                                     Other;
                                                                                             Length
                                                           Indels
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                                                         Gaps
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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26-JUL-2000,
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14-JUL-2000
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24-FEB-2000;
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2000US-0225266P.
2000US-0225275P.
2000US-022575P.
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2000US-0227182P.
2000US-0227892P.
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2000US-0189874P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen
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lne; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cc example, the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) concleic acids into a host cell and culturing the cell to express the cc protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the ccl cancers and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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17-NO
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08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43938 BP; 12772 A; 9656 C; 9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 32028; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483426/52.
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2000US-02511899P.
2000US-02511899P.
2000US-02511989P.
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                                                                                                                                                                                                                                                                                                                                                                                                                           21.1%; Score 39.8; DB 4; 32.2%; Pred. No. 0.69; tive 34; Mismatches 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and metastasis.
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01-SEP-2000
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02-OCT-2000
02-OCT-2000
03-NOV-2000
08-NOV-2000

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2000US-0246532\$P.
2000US-024653

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RESULT 8
ID X77217
ID X777217
AC AAK77217
AC AAK77
AC AAAK77
AC AAAK77
AC AAAC77
A
  11-APR 2000
19-MAY 2000
19-MAY 2000
19-MAY 2000
28-JUN 2000
28-JUN 2000
07-JUL 2000
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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  2000US-018464P.
2000US-0189874P.
2000US-0189874P.
2000US-0198135P.
2000US-0205515P.
2000US-0201886P.
2000US-0211886P.
2000US-0211886P.
2000US-0211887P.
2000US-0211889P.
2000US-0211899P.
2000US-0211899P.
2000US-0224519P.
2000US-0225213P.
2000US-0225213P.
2000US-0225213P.
2000US-0225266P.
2000US-02252679.
2000US-0225759P.
2000US-0235759P.
2000US-
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2000US-0180628P
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        21-SEP-2000

25-SEP-2000

25-SEP-2000

26-SEP-2000

27-SEP-2000

29-SEP-2000

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14-SEP-2000
2000US-0232081P.
2000US-0232396P.
2000US-0232396P.
2000US-0232396P.
2000US-0233063P.
2000US-0233063P.
2000US-0233063P.
2000US-0234274P.
2000US-0234274P.
2000US-0235834P.
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2000US-0246478P.
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC concers and treat immune/haematopoietic related diseases, especially CC diagnose and treat immune/haematopoietic related diseases, especially CC cancers and cancer metastases of haematopoietic derived cells. AAK64703 CC cancers and cancer metastases of haematopoietic derived cells. AAK64703 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
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Best Local S
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05-DEC-2000;
06-DEC-2000;
   Cytostatic;
                                    Human cancer associated sequence HD10-002, SEQ ID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45017 BP; 12919 A; 10037 C; 9566 G; 12495 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 32029; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasi
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                                                                                                                                          ADQ97028 standard; DNA; 84476
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       8574 TCATCTCGGGTCTTAAAATAAAATTCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA
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                                                                                                                                                                                                                                                                                                                                    UAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUC 129
                                                                                                                                                                                                                                                                                                                                                                                                         caegacacccucucuecuucuuauaueauuaeeuueucauuuaeaauaaea 180
                                                                                                                                                                                                                                Barash SC,
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2000US-0251856P.
2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
2000US-0251999P.
2000US-0254997P.
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; 2000US-0250391P.
; 2000US-0251030P.
; 2000US-0251988P.
; 2000US-0256719P.
Gene Therapy; cancer; leukemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        21.1%; Score 39.8; DB 4; Length 45017;
32.2%; Pred. No. 0.69;
tive 34; Mismatches 82; Indels 0;
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                                                                                                                                          ВP
   Human;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 7087.
                                  23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                     23-MAR-2001; 2001WO-US009231.
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                                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83402 TCATCTCGGGTCTTAAAATTAAAATTCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 5059 BP.
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32.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39.8; DB Pred. No. 0.79;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL30511), expressed DNA sequences (ABL16196-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                         30-JUL-2001; 2001US-00918995
                                                                                                                 17-APR-2003.
                                                                                                                                        US2003073623-A1
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                         genome
                                                                                                                                                                                                                              Human foetal brain cDNA #6596.
                                                                                                                                                                                                                                                       13-OCT-2003
                                                                                                                                                                                                                                                                                ACH45871
                                                                                                                                                                                                                                                                                                         ACH45871 standard; cDNA; 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5059 BP; 1352 A; 1177 C; 1183 G; 1347 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 7087; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes from Drosophila
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  (DRMA/)
(LABA/)
(STAC/)
(DICK/)
                                                                30-JUL-2001; 2001US-00918995.
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                                                                                                                                                                                        ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
mapping; biodiversity; genetic disorder.
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57; Conserv
                           DRMANAC R T.
LABAT I.
     DICKSON M C.
                 STACHE-CRAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.6; DB Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                ALPV; ; aphid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probbes, as oligomers for PCR, for chromosome and cane marrian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide comprising any 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequent determined by the technique of SBH (sequencing by hybridisation). I
                                                                                                                                                                                                                                                                                                                                                                                                       Aphid lethal
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                                                                                                                                                                                                                                                                                                                Aphid lethal paralysis virus; white fly; agriculture; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 UAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ИЗАИСИИЗСИИССИИАИАСАЛИИИИЗАКАСБИИЛАИЛАВАЛОВАЛОВСИИИСИИЛА
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                                                                                                                                                                                                                                                          paralysis virus
                                                                                                                                                                                                                                                                                                                                                                                                       paralysis virus (ALPV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                      therapy;
                                                                                                                                                                                                                                                                                                                                                    homopterous insect;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 460;
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25-OCT-2001; 2001NL-01019225 25-OCT-2002; 2002WO-NL000682

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Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel RNA derived from an ALPV (Aphid lethal paralysis virus). ALPV RNA is useful for controlling homopterous insects such as aphids or white flies. It is useful in the research concerning aphids and for controlling aphids and in the field of agriculture or floriculture. It is also useful for detecting ALPV- viruses using PCR and for preparing a monoclonal antibody against antigen which is synthesised in vitro. The invention is also useful in gene therapy. The present
                                                                          Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translactivity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudoknot; secondary structure; cell-free protein synthesis; wheatgerm, albumen; impurity; higher-order structure; intergenic region; IGR-IRES; internal ribosome entry site; ss.
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                              Claim
                                                                                                                                                                                       WPI; 2003-403230/38
                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2001; 2001JP-00319923.
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                                                                                                                                                                                                                                      Nakashima N,
                                                                                                                                                                                                                                                                                             (WAKE-)
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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Triatoma virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                           Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                 CrPV-like virus; ss; higher-order structure; drug drug production; translational activity-promoting
                                                                                                                                                                                                                                                                                31-JAN-2001; 2001WO-JP000641
                                                                                                                                                                                                                                                                                                          08-AUG-2002
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                                                                                                                                                                              WPI; 2002-627482/67
                                                                                                                                                                                                       Nakashima N,
                                                                                                                                                                                                                                                        25-JAN-2001; 2001JP-00016746.
                                                                                                                                                                                                                                                                                                                                  WO200261080-A1.
                                                                                                                                                                                                                                                                                                                                                             Triatoma virus.
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                                                                                                                                                                                                                                                                                                                                                                                     synthesis; structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAAGAUCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCA 119
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                                                                                                                                                                                                       Kanamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA; 198
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Pred. No. 1.8;
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The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of protesins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in

of protein

synthesis and structural

Claim 1; Fig

1-2;

38pp; Japanese.

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RESULT 15
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                                                   The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the himetobi P virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing useful proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Himetobi P virus derived pseudoknot sequence.
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   Sequence 187 BP; 53 A; 32 C; 39 G; 0 T;
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 32; 39pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUAAUAUCCAGG 133
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ilarity 59.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nishikawa S;
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Query Match

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                                                                        54 AGUAGUGCUAUCUUAAUAAUUAGGUUAACUAUUUAGUUUVACUGUUCAGGAUGCCUAUUG
                                                                                                             63;
GCGUUCCUGCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAG
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4471.109 Million cell updates/sec
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A CZ311732
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CO153155 EN01401.5
CO153154 EN02010.5
CO153765 EN02756.5
CO153765 EN02756.5
CO337794 EN15321.5
CO338064 EN15825.5
CO338705 EN15125.5
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CO22498 WS01026. B
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CC3338852 ZMMHBF0107
AG520404 Mus muscu
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CN254287 B1P0433 B
CN254287 B1P0433 B
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| 35 | 35.2 | 35.2 | 35.2 | 35.2 | 35.4 | 35.6 | 35.6 | 35.8 | 35.8 | 36 | 36 | 36 | 36 | 36 | 36 | 36.2 | 36.2 | 36.2 | 36.2 | 36.4 | 36.4 | 36.4 |
| 18.5 | 18.6 | 18.6 | 18.6 | 18.6 | 18.7 | 18.8 | 18.8 | 18.9 | 18.9 | 19.0 | 19.0 | 19.0 | 19.0 | 19.0 | 19.0 | 19.2 | | 19.2 | | 19.3 | 19.3 | 19.3 |
| 364 | 975 | 789 | 784 | 675 | 907 | 921 | 769 | 978 | 284 | 1039 | 684 | 682 | 563 | 547 | 541 | 816 | 814 | 811 | 394 | 1057 | 925 | 842 |
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| BZ216751 | DN562098 | CK316785 | CB199345 | AZ527316 | DU002474 | CL099026 | BZ489474 | CC717480 | BI691829 | CG418022 | CZ783049 | BM168656 | CZ705112 | CD451731 | AQ419640 | CC546802 | CC972368 | BZ385506 | BF908674 | CL997184 | CZ506071 | CC070286 |
| BZ216751 CH230-250 | DN562098 90906553 | CK316785 SB02019B2 | CB199345 AGENCOURT | AZ527316 267PbB02 | DU002474 284709 To | CL099026 ISB1-32B1 | BZ489474 BONFG30TF | CC717480 OGPAJ63TV | BI691829 603307551 | CG418022 ZMMBBc002 | CZ783049 OCBa014 | BM168656 EST571179 | CZ705112 OC Ba002 | USDA- | AQ419640 RPCI-11-1 | CC546802 CH240_429 | CC972368 ZUAEX42TV | BZ385506 B15.874ST | BF908674 IL2-UT007 | CL997184 ZMMBHf001 | CZ506071 GMW2-13B1 | CC070286 CSU-K33r. |

ALIGNMENTS

| Qy Db | Query Match Best Local & Matches 120 | ORIGIN | FEATURES BOUICE | REFERENCE AUTHORS TITLE JOURNAL COMMENT | RESULT 1 CO153155 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM |
|---|---|--|---|---|--|
| 1 GUUAAGAUGUGAUCUUGCUUCCUUAUACAAUUUUGAGAGGUUAAUAAGAAGGAAG | Query Match 99.2%; Score 187.4; DB 7; Length 433; Best Local Similarity 63.5%; Pred. No. 1.2e-41; Matches 120; Conservative 68; Mismatches 1; Indels 0; Gaps 0; | /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="caxon.7227" /clone="EN01401" /clone="EN01401" /cell_line="mbn2" /cell_line="mbn2" /clone_lib="Exelixis FlyTag MN08 BlueScript" /note="Wector: pBluescript; Site_1: NotI; Site_2: XhoI; oligodT primed from LPS induced mbn2 cell line." | BDGP Lawrence E One Cyclot Fax: 510 4 Email: htt Plate: EN High quali | Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 433) Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Platt, D. and Swimmer, C. and Swimmer, C. Exelixis FlyTag EST Project MN08 Library Unpublished (2004) Contact: Stapleton, M. | CO153155 433 bp mRNA linear EST 05-OCT-2004 EN01401.5prime Exelixis FlyTag MN08 BlueScript Drosophila melanogaster cDNA clone EN01401 5, mRNA sequence. CO153155 CO153155.1 GI:48907156 EST. Drosophila melanogaster (fruit fly) Drosophila melanogaster (fruit fly) Brosophila melanogaster Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterycota; Diptera; Brachycera; Muscomorpha; |

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REFERENCE
AUTHORS
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SOURCE
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VERSION
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CO153454
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                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 486)
1 (bases 1 to 486)
Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Plandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, M., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, M., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, M., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, M., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, M., Pandarishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, M., Pandarishi, M., Muzong, C., Peterson, E., Laufer, M., Pandarishi, M., Panda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EN.20 row: A column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exelixis FlyTag EST Project MN08 Library
Unpublished (2004)
Contact: Stapleton, M.
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CO153454.1 GI:48907455
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                                                    AAATAACCT 253
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/note="Vector: pBluescript; Site_1: NotI; Si
oligodT primed from LPS induced mbn2 cell li:
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/db_xref="taxon:7227"
/clone="EN02010"
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/mol_type="mRNA"
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CO153765
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                                                                                                                                                        CO337794
EN15317.5prime Exelixis F
melanogaster cDNA clone E
CO337794
CO337794.1 GI:49398069
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                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 490)
Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, Plate: EN.27 row: E column: 8 High quality sequence stop: 401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATAACCT
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Swinmer,C.
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oligodT primed from LPS induced mbn2 cell line."
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63.5%; Pred. No. 1.2e-41;
cive 68; Mismatches 1;
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Berkeley, CA 94720, USA
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FlyTag MN08 BlueScript Drosophila
EN15317 5, mRNA sequence.
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BlueScript Drosophila
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                                                             Pterygota;
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Matches 12
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                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 453)
Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pl.
                                                                                                                                                                                                                              and Swimmer,C.
Exelixis FlyTag EST Project MN08 Library
Innublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CO338064 453 bp mRNA linear EST 0: EN15862 5prime Exelixis FlyTag MN08 BlueScript Drosophila melanogaster cDNA clone EN15862 5, mRNA sequence. CO338064 CO338064.1 GI:49398359 EST.
                  Lawrence Berkeley National Lab one Cyclotron Rd, Berkeley, CA 94720, Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, esplate: EN.158 row: F column: 2 High quality sequence stop: 399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: EN.153 row: B column: 5 High quality sequence stop: 474.
                                                                                                                                                                                                                         Contact: Stapleton, M.
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Plate: EN.153 row: B column: 5
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One Cyclotron Rd, Berkeley, CA
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/clone_lib="Exclixis FlyTag MNO8 BlueScript"
/clone_lib="Exclixis FlyTag MNO8 BlueScript"
/note="Vector: pBluescript; Site_1: NotI; Site_2:
/note="Vector: pBluescript; Site_1 NotI; Site_2:
/note="Vector: pBluescript; Site_1 NotI; Site_2:
/note="Vector: pBluescript; Site_2: NotI; Site_2: NotI
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(mol_type="mRNA"
/db_xref="caxon:7227"
/clone="EN15317"
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Pred. No. 1.2e-41;
8; Mismatches 1;
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                                                                                                 est@fruitfly.berkeley.edu
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Best Local Similarity
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  CO224988
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 472)
1 (bases 1 to 472)
Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pl.
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EN15125.5prime Exelixis FlyTag MNO8 BlueScript Drosophila
melanogaster cDNA clone EN15125 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, Plate: EN.151 row: C column: 1 High quality sequence stop: 360.
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היים ריירוסtron Rd, Berkeley, CA 94720,
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                                                                                               /clone lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site_1: NotI; Site_2
oligodT primed from LPS induced mbn2 cell line."
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/clone lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site_1: NotI; Site_2:
oligodT primed from LPS induced mbn2 cell line."
                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/mol type="mRNA"
/db_xref="taxon:7227"
/clone="EN15125"
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|mol type="mRNA"
|db xref="teaxon:7227"
|clone="EN15862"
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                                                                                                                                                                          Score 48; DB 7;
Pred. No. 0.011;
9; Mismatches
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Pred. No. 2.8e-08;
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Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ralph,S., Kolosova,N., Oddy,C., Cooper,D., Butterfield,Y., Yang,G., Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John, Chand,S., Feathestone,R., Masson,A., Mayo,M., Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.
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1 (bases 1 to 448)
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Plate: WS01026 row: D column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries
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AGTTATTTAACTTTACTTATCAAGATGGCCCCAGGCAGCCCCTGAAAATCTAG
                                                                                                            AACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUCCAG 132
                                                                                                                                                                                                                                                                                                                                    ОССОПАНАСА ПОПИСА В ПОПИСКО В ПО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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/clone="WS01026_D16"
/sex="Hermaphrodite"
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/cultivar="Gb2-229"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                       Mus musculus (house mouse)
                                                                                                   GSS.
                                                                                                                                      genomic survey sequence AZ748753
                                                                                                                                                                          RPCI-24-65N21.TJ RPCI-24
                                                                                                                  AZ748753.1 GI:12533912
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BAC end sequencing from three Solanum lycopersicon libraries
Unpublished (2005)
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CZ956789
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: sgn-feedback@sgn.cornell.edu Plate: 65 row: P column: 3
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Tel: 607-255-6557
Fax: 607-255-6683
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Tanksley Lab, Dept. of Plant Breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller, L.A.,
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                                                                                                                                                                                                                                                                                                                                                                UAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUCCAGGACACCCUCU 142
                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAATCCACTTTGAATTAACAACAATATTGACTTATTTCTATAATTATTATGAAACTATA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UUAUACAAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUCUUAAUAAUUAGGUUAAC 82
                                                                                                                                                                                                                                                                                       TTGTTTTTTÄTÄCGÄCGÄGCTTTTČCTGTTAÄÄTÄTAÄCTÄATTČČT
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/lab_host="E. col1"
/lab_host="F. col1"
/clone lib="Tomato EcoRI BAC Library"
/note="Vector: unk; Site_1: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon
/mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%; Score 42.2; DB 10; 29.9%; Pred. No. 0.51; tive 39; Mismatches 78;
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RPCI-24-65N21,
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Mouse BAC and Sequences from Library RPCI-24
Unpublished (199)
Other, GSSs: RPCI-24-65N21.TV
                                                                                                                        survey sequence.
CZ338852
CZ338852.1 GI:6
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse bacter de Jong
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 65 row: N column: 21
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/clone_lib="RPCI-24"
/clone_lib="RPCI-24"
/note="Vector: pdfBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pdfBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pdfBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pdfBAC1; Site_2: BamH1; Site_2: BamH1; Sites using MboI partially digested male C57BL/6J
BamH1 sites using MboI partially digested male C57BL/6J
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/strain="C57BL/6J"
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,Cand Messing,J.
Construction, Sequencing and Characterization of a Fosmid Library
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
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Hattori, M., Toyoda, A.,
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Shiroishi, T.
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The Plant Genome Initiative at
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                 BIP0018 BIP up-regulated phloem library after plant infestation with Myzus persicae Apium graveolens cDNA, mRNA sequence. CN253956 CN253956.1 GI:51972432
                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Apiales; Apiaceae; Apioideae; apioid superclade; Apium clade; Apium.

1 (bases 1 to 351)

1 (bases 1 to 351)

1 (bolon, Vilaine, F., Thibivilliers, S., Amselem, J., Palauqui, J.C., Kusiak, C. and Dinant, S. Kusiak, C. and Dinant, S. Systemic response to aphid infestation by Myzus persicae in the phloem of Apium graveloens

Plant Mol. Biol. 57 (4), 517-540 (2005)
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                            Apium graveolens
Apium graveolens
                                 Laboratoire de Biologie Cellulaire
                                                   Contact: Dinant
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LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity 30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAUAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUAAUAUCCAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUUAGAAUAAGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAATTATTAAGAAATATTATATGTTATATTTGTAAAATAAAATTACGTTTGTATAAAAT 1452
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de
St-Cyr 78026
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/mal_type="genomic DNA"
/sub_specise="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="mixture of kidney and spleen"
/clone_Tib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="MSMg01-427C02.T7"
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EcoRI
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Versailles Cx France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (abe@rtc.riken.jp).
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PUBMED
COMMENT
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CN254287
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Best Local &
                                                                  source
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                                                                                                                     Tel: 33130833047
Fax: 33130833099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN254287.1
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Fax: 33130833099
                                                                                                                                                                                                          Contact: Dinant
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                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Vert_d'Elne"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:51972763
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214 ATATCAAATGTCGTTAATTGGTTAGGTAGCTATTAACGTCAGAAATTTACCT
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351 bp mRNA linear EST 10-SEP-:
BIP0433 BIP up-regulated phloem library after plant infestation
with Myzus persicae Apium graveolens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                    superclade; Apium clade; Apium.

1 (Dases 1 to 351)
Divol,F., Vilaine,F., Thibivilliers,S., Am
Kusiak,C. and Dinant,S.
Systemic response to apind infestation by
phloem of Apium graveloens
Plant Mol. Biol. 57 (4), 517-540 (2005)
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Apium graveolens
Apium graveolens
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Eukaryota, Magnoliophyta, eudicotyledons; core eudicotyledons;
Spermatophyta, Magnoliophyta, eudicotyledons, apioideae; apioid
                                                                                                                                                                                                                                          Route de St-Cyr 78026 Versailles Cx France
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                                                                                                                                                                                                                                                                                                   Laboratoire de Biologie Cellulaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAAUAACCU 189
                                                                                                                                                   Sylvie.Dinant@versailles.inra.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="BIP up-regulated phloem library after plant infestation with Myzus persicae" /note="Vector: pCRII-TOPO; Substractive library (SSH) enriched in cDNA coming from Apium graveolens phloem tissue and up-regulated by Myzus persicae infestation. This sequence has been generated in the framework of the French plant genomics program Genoplante (http://www.genoplante.org and http://genoplante-info.infobiogen.fr)."
/organism="Apium graveolens"
/mol_type="mRNA"
/cultivar="Vert d'Elne"
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/dev_stage="adult plant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thibivilliers, S., Amselem, J.,
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Pred. No. 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Palauqui, J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 10-SEP-2004
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RESULT 14
CL045570
LOCUS
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ORGANISM
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VERSION
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Best Local S
Matches 53
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 ATATCAAATGTĆGTTAÁTTGGTTAĠGTAGĆTATTÁACGTCÁĠÁÁATTTÁĆĆT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 UUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUCCAGGACAC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CL045570 1088 bp DNA linear GSS 31-DEC-2003 CH216-63A10_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-63A10, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kremitzki,C., Carter,J., McPherson,J., Warren,W., Mardls,E. and Wilson,R.
A physical map of the xenopus tropicalis genome Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS.
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CL045570.1 GI:40501483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 1088)
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Similarity 30.8%;
53; Conservative 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence start: 16 quality sequence stop: 764 Location/Qualifiers
                                                                                                                                                                                                         /organism="Xenopus tropicalis"

/mol_type="genomic DNA"

/strain="Nigerian frog"

/db xref="taxon:8364"

/clone="CH216-63A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              French plant genomics program Genoplante (http://www.genoplante.org and http://genoplante-info.infoblogen.fr)."
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                                                                                                             /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 X
                                                                                                                                                                                          sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="phloem"
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                                                                                                 library"
20.4%;
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Score 38.6; I Pred. No. 5.3;
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                      DB 10;
                                                                                                                CHORI-216 Xenopus tropicalis
                        Length 1088;
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 1 Similarity 47; Conserv
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                                                                                                                                                                                                                                                                                   R.Site 1
R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                                           Tibrary availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/Tel:81-45-503-9170, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
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Shiroishi, T
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                                                                                                                                                                                                                                                                                                                                                                                                 e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
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Genome Res. 14 (12), 2
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Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y.,
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 Conservative
                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                          tissue_type="mixture of/clone_lib="MSMg01 Mouse
                                                                                                                                                 /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-305B16.T7"
                                                                                                                                                                                                                          organism="Mus musculus molossinus"/
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 Score 38.4; D
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Moriwaki, K.
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Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/B_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PE_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*
99.2 1345
99.2 1784
21.1 54444
18.9 1788
18.3 4486
17.2 294836
17.0 365407
17.0 139150
17.0 13957
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17.0 807
18.8 67876
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Gapop 10.0 , Gapext 1.0
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             US-09-270-767-1072
US-09-249-016-17344
US-09-249-016-17344
US-09-248-796A-6320
US-08-322-742-15
US-08-322-742-15
US-08-949-016-15974
US-09-949-016-17543
US-09-949-016-12879
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US-09-949-016-12732
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US-09-949-016-1173344
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Sequence 16354, A
Sequence 17344, A
Sequence 6320, Ap
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  15, Appl
15974, Appl
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17543, Appl
2, Appl
17398, A
12979, A
12979, A
12979, A
12979, A
129290, A
1733, Appl
1733, Ap
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1072
LENGTH: 1345
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| 30.6 | 30.6 | 30.6 | 30.6 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 |
| 16.2 | 16.2 | 16.2 | 16.2 | 16.3 | | 16.3 | 16.3 | 16.3 | 16.3 | 16.3 | | 16.4 | 16.4 | 16.4 | 16.4 | 16.4 | 16.4 | 16.4 | 16.4 |
| 3228 | 601 | 333 | 321 | 181430 | 181429 | 8546 | 8546 | 6294 | 6294 | 672 | 640681 | 174318 | 174318 | 174318 | 174170 | 174170 | 140315 | 121234 | 108060 |
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| US-09-710-279-3643 US-09-710-279-3808 | US-09-949-016-60132 | US-09-134-001C-1242 | US-09-710-279-1161 | US-09-949-016-15772 | US-09-949-016-12372 | US-09-949-016-16049 | US-09-949-016-15114 | US-09-956-004-5 | US-08-976-259-5 | US-09-601-198-157 | US-09-790-988-1 | US-09-949-016-14813 | US-09-949-016-14812 | US-09-949-016-11880 | US-09-949-016-14811 | US-09-949-016-14810 | US-09-949-016-14141 | US-09-949-016-14142 | US-09-949-016-13159 |
| Sequence 3643, Ap Sequence 3808, Ap | ,2 | Sequence 1242, Ap | Seguence 1161, Ap | Sequence 15772, A | Sequence 12372, A | Seguence 16049, A | Sequence 15114, A | Sequence 5, Appli | Sequence 5, Appli | Sequence 157, App | Sequence 1, Appli | Sequence 14813, A | Sequence 14812, A | Sequence 11880, A | Sequence 14811, A | Sequence 14810, A | Sequence 14141, A | Sequence 14142, A | Sequence 13159, A |

ALIGNMENTS

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RESULT 2
US-09-270-767-16354
US-09-270-767-16354
; Sequence 16354, Application US/09270767
; Patent No. 6703491
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1072
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Similarity 63.5%; Pred. No. 2.3e-47;
20; Conservative 68; Mismatches 1; Indels 0;
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; ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRSESEQ for Windows Version 4.0
SEQ ID NO 17344
LENGTH: 54444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16354
LENGTH: 1345
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local Similarity
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                 V Match 21.1%; Score 39.8; DB Local_Similarity 32.2%; Pred. No. 0.055;
                                                                  43694 TCATCTCGGGTCTTAAAATAAAATCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA 43635
     43574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATTTTAATAATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCTATTGGCAGCCC 636
                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09949016
                                                                                                                                                                                                                    34; Mismatches
                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                 Length 54444;
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CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6320
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6320
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US-08-322-742-12/c
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US-09-248-796A-6320/c
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PATENT NO. 6747137
GENERAL INFORMATION:
APPLICANT: Kelth Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08322742 Patent No. 5688641 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                APPLICATION NUMBER: US/08/322,74
FILING DATE:
RETOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: September 1,1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/852,216
ETITM DATE: February 28, 1992
APPLICATION NUMBER: 07/852,216
                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                           FILING DATE: February 28
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sager, RUTITLE OF INVENTION: NUMBER OF SEQUENCES:
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TELEPHONE: (617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
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225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANCER DIAGNOSIS AND THERAPY
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                                                                  00530/048003
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4328

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                                                     ; STRANDEDNESS: , TOPOLOGY: 11: US-08-322-742-15
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Patent No. 5688641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Query Match
Best Local Similarity
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APPLICANT: Sager, Ruth
TITLE OF INVENTION: CA
                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: E1-1.
                                                                                                                                                                                                                                                                                                          FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: IBM P.C. DOS (Ver
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,742
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55S;
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4486
                                                                                                                                                                                                                  REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/048003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                           NAME: Fraser, Janis K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2175 ATAAATGCATAGCAATGTTTCATGAAAACCATGCAAATTATAAAAACAA 2127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 GACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAA 181
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                                                                                                       nucleic acid
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                                                                                                                                                                                                 (617) 542-8906
                                                                        linear
                                                                                        double
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 18.3%;
27.2%;
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Pred. No. 0.97;
 Score 34.6; DB Pred. No. 0.98;
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                   Length 4486;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498
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Patent No. 6812339
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Best Local S
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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TYPE: DNA
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NAME/KP: misc_feature

LOCATION: (1)...(294836)

OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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; Sequence 2, Application US/09692570 ; Patent No. 6797466
                                                               RESULT 10
US-09-692-570-2
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US-08-916-4218-2
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; ORGANISM: Human
US-09-949-016-17543
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APPLICANT: Bult et al.
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows
SEQ ID NO 17543
LENGTH: 36546
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Best Local Similarity
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SEQ ID NO 2
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TITLE OF INVENTION: jannaschii
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NAME/KEY: misc feature
LOCATION: (6485)..(6485)
OTHER INFORMATION: n equals a, t, c,
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CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
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TYPE: DNA
ORGANISM: Methanococcus jannaschii
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Pred. No. 10;
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GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence
Patent No. 6797466
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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Matches
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SEQ ID NO 2
LENGTH: 58407
                                                                                                                                           SEQ ID NO 17398
LENGTH: 139150
Matches
                   Best Local
                                       Query Match
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ORGANISM: Methanococcus jannasch
FEATURE:
NAME/KEY: misc feature
LOCATION: (6485)..(6485)
OTHER IMPORMATION: n equals a, t
                                                                                                                                                                                    PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows
                                                                                                                         TYPE: DNA
                                                                                                      ORGANISM: Human
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                   Similarity
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Conservative
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                                                                                                                                                                                      Windows Version
17.0%; Score 32.2; I 23.7%; Pred. No. 15; tive 33; Mismatches
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Gaps
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
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; ORGANISM: Human
US-09-949-016-12879
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                        NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRETSEQ for Windows Version 4.0
SEQ ID NO 12928
LENGTH: 194537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12879
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Best Local Similarity
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                                               ORGANISM: Human
                                                                         TYPE: DNA
NAME/KEY: misc_feature
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Pred. No. 15;
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; ORGANISM: Human
; FEATURE;
; NAME/KEY: misc feature
; LOCATION: (1)...(201529)
; OTHER INFORMATION: n = A,7
US-09-949-016-12740
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US-09-949-016-12740
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                                                                                                                                                                                                                                                  US-09-299-378-3
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12740
                                                                                                                                                                                                     Sequence 3, Application US/09299378 Patent No. 6245545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12740,
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Best Local :
FILE REFERENCE: SWAI
CURRENT APPLICATION NUMBER: US/09/299,378
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 20
                                                                           APPLICANT: Higgins, Lauren S.
APPLICANT: Dalton, Michael A.
APPLICANT: Kong, Huimin
TITLE OF INVENTION: Method For Cloning And
TITLE OF INVENTION: Endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                               183390 GCTTACATGTACAATTAAGAAAGTTTAATAAAAACAAGATAATTGTTTACTCAATGTGGG 183449
                                                                                                                                                                                                                                                                                                                               183450 GTGÄATAAGTGÄGTGATAGCAGTCATGGTGGTGGGTGGGTTAAATCAAAGTATAAATG 183506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176450 GTGÄÄTAAGTGAGTGATÄGCAGTCATGGTGGTGGGGTTAAATCAAAGTATAAATG 176506
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Local Similarity 34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.0%; Score 32.2; 34.2%; Pred. No. 17;
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Pred. No. 17;
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                   Score
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seq length: 2000000000
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq: *

2: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq: *

3: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq: *

4: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq: *

5: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq: *

6: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq: *

7: /cgn2 6/ptodata/1/pubpna/US108 PUBCOMB.seq: *

9: /cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq: *

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10: /cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq: *
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Copyright (c) 1993 - 2005 Compugen Ltd.
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7 US-10-088-750B-3

7 US-10-088-750B-4

7 US-10-088-750B-6

10 US-11-097-143-25048

US-09-918-995-33083

10S-09-925-065A-38108

10S-10-088-750B-2

10S-10-088-750B-2

10S-10-088-750B-2

10S-10-195-144-87

10S-10-195-144-87

10S-10-345-072-87

10S-10-345-073-108

10S-10-313-455-448

10S-10-311-455-448

10S-10-240-485-173

10S-10-240-485-173

10S-10-225-065A-5345876

10S-10-225-065A-5345876

10S-10-240-485-173

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10S-10-240-485-173
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                Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 3003, A
Sequence 38107, A
Sequence 38108, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 694931,
Sequence 697, Ap
Sequence 87, Appl
Sequence 108, Appl
Sequence 118, Appl
Sequence 1, Appl
Sequence 331874,
Sequence 348, App
Sequence 403, App
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| 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.6 | | 32.6 | 32.6 | 32.6 | 32.6 | (1.0 |
| 17.0 | 17.0 | 17.0 | 17.(| 17.0 | 17.0 | 17.0 | 17.0 | 17.0 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | |
|) 1532 | 622 | 622 |) 556 |) 556 | 281 | 201 | 201 | 200 | 256190 | 9760 | 9642 | 6815 | 6815 | 6815 | | 15932 | 600 | 592 | 592 | 501 | |
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| US-09-925-065A-691288 | US-09-925-065A-144314 | US-09-925-065A-144313 | US-09-925-065A-626880 | US-09-925-065A-626879 | US-10-088-750B-10 | US-10-741-600-60756 | US-10-741-601-21466 | US-10-088-750B-1 | US-10-322-281-320 | US-10-221-613-114 | US-10-311-455-330 | US-10-240-453-49 | US-10-311-455-643 | US-10-239-676-49 | US-10-311-455-1388 | US-10-741-600-17599 | US-10-972-079-75861 | US-09-925-065A-98096 | US-09-925-065A-98095 | US-10-972-079-75862 | |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | |
| 691288, | 144314, | 144313, | 626880, | 626879, | 10, Appl | 60756, A | 21466, A | 1, Appli | 320, App | 114, App | • | 49, Appl | | 49, Appl | 1388, Ap | 17599, P | 75861, 7 | 98096, A | 98095, A | 75862, A | |

ALIGNMENTS

Sequence 3, Application US/10088750B Publication No. US20040166486A1 GENERAL INFORMATION: APPLICANT: NAKASHIMA, Nobuhiko APPLICANT: KANAMORI, Yasushi TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation TITLE OF INVENTION: Activity FILE REFERENCE: 3190-015 CURRENT APPLICATION NUMBER: US/10/088,750B CURRENT APPLICATION NUMBER: JP P2001-016746 PRIOR APPLICATION NUMBER: PCT/JP01/00641 PRIOR APPLICATION NUMBER: PCT/JP01/00641 PRIOR FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 12 SOFTWARB: Patentin version 3.2 뫄 밁 δ S 밁 US-10-088-750B-3 US-10-088-750B-3 Query Match Best Local Similarity Matches 189; Conserv SEQ ID NO 3 LENGTH: 201 TYPE: RNA ORGANISM: Drosophila C Virus 181 121 61 61 CAUAAUAUCCAGGACACCCUCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGA CUAUCUUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCC 120 AAAUAACCU 189 CUAUCUUAAUAAUUAGGUUAACUAUUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCC 120 CAUAAUAUCCAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGA Conservative 100.0%; Score 189; DB 7; 100.0%; Pred. No. 4.1e-44; tive 0; Mismatches 0; Length 201; Indels 0 180 180 60

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Sequence 6, Application US/10088750B

Publication No. US20040166486A1

GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: NAKASHIMA, Nobuhiko
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR RILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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ITITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
ITITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
ITITLE OF INVENTION: Activity
PILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT APPLICATION NUMBER: UP 2001-016746
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
INUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 200
CURRENT APPLICATION OF SEQ ID NOS: 12
SOFTWARE: Cricket Paralysis Virus
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                                                                                 Query Match
Best Local
                                                      Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10088750B Publication No. US20040166486A1
                                                                                                                                                                  TYPE: RNA
ORGANISM: Black Queen-Cell Virus
                                                                                                                                                                                                                  LENGTH: 202
                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 АНИАИССАСБАСАСССИСИСИСИИСИИАИАИБАИИАСБИИСИСАВИИНАБААИАБВАДА 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 UAACCU 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 ИСИЛААПЛАНИЯ В 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUGUGAUCUUGCUUCCUUAUAC-AAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAU 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UUACCU 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAUGUGAUCUUGCUUGUAAAUACAAUUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UUUUUGUAUUUAGGUUAGCUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCAC 122
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                          24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%; Score 123.6; DB 7; 79.0%; Pred. No. 2.4e-25; vative 0; Mismatches 39;
                                               Score 45.4; DB 7;
Pred. No. 0.0066;
0; Mismatches 71;
                                                                                          Length 202;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 200;
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APPLICANT: Venter, J. Craig
APPLICANT: Vet al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NU
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXX
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOO0728
FILE REFERENCE: CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
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US-11-097-143-25048/c
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LENGTH: 5059
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25048, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                 481 AA 480
                                           182 AA 183
                                                                                                                        122 АИААИАИССАВСАСССИСИСИССИСИИЛИЛИВИНИВОВИИЗОСЛИВИНАВАЛИЛАВАЛ 181
                                                                                                                                                                                                      62 UAUCUUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAAUUU 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                            66 UUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAU-UGGCAGCCCCAUA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                  TAAACATCAATGTTAATCTTGTTGCTGCTAACATTTTAATGTTATGTTATCGAAAAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUC
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                                                                                                                                                                                                                                                                                                                                          21.0%; Score 39.6; DB 10; ilarity 31.3%; Pred. No. 1; Conservative 36; Mismatches 89;
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EXPRESSION OF 10,000
                                                                                                                                                                                                                                                                                                                                                                                   Length 5059;
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RESULT 5 US-09-918-995-33083

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(460)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-33083
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR ETILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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                                                US-09-925-065A-38107
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Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38107
LENGTH: 2360
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33083
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
Query Match
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CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR PILING DATE: 1999-01-20
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                LENGTH: 2360
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 CAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 TCATCTCGGGTCTTAAAATTAAAATTCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 UAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Conservative
19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Mismatches
  Score 37.4;
  DB 4;
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Length 2360;
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                                                                                                                                                                                                                                                             RESULT 8
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; ORGANISM: Homo sapiens
US-09-925-065A-38108
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR TILING DATE: 2000-10-24
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
Sequence 5, Application US/10088750B
Publication No. US20040166486A1
GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
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SEQ ID NO 38108
LENGTH: 2360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                    1386 CTTCCTCTGGAATAA 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                     1326 GAGAAATATAAAAGACACTACATTTCTAGGAAGAAACAGCTGAACAATAGATTAGCCATT 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1266 ATAACAGGGAAATATAACTACCTAAATAATTTTGTTTATAATTTAGTCCTACCGTTTATA 1325
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                                                                                                                                                                                                                                                                                                                                                                                      164 UGUCAUUUAGAAUAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 UGUCAUUUAGAAUAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AUGCCUAUUGGCAGCCCCAUAAUAUCCAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGU 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 AUGCCUAUUGGCAGCCCCAUAAUAUCCAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGU 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 AUAAGAAGGAAGUAGUGCUAAUCUUAAUUAGUUUAACUAUUUAGUUUUACUGUUCAGG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.8%; Score 37.4; DI 34.8%; Pred. No. 3.3; ative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Indels
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CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
UMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN VEXESON 3.2
SEQ ID NO 2
RESULT 10
US-09-925-065A-694931
; Sequence 694931, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
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                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: Himetobi P Virus
US-10-088-750B-2
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                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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ORGANISM: Triatoma Virus
-10-088-750B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR APPLICATION NUMBER: PCT/JP01/00641
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 3190-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 199
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Local Similarity 59.8%;
les 79; Conservative
                                                                                                                                                                              114 GCAGCCCAUAAUAUCCAGGACACCCUCUCUGCUUCUUAUAUAUGAUUAG 161
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Pred. No. 3.3;
0; Mismatches 4
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US-10-719-993-6967
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6967
LENGTH: 142947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6967, Application US/10719993 Publication No. US20040265849A1 GENERAL INFORMATION:
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                                                                                                                                             Matches
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(142947)
OTHER INFORMATION: n = A,T,C or G,
                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 TITTATAGTITITCAAGAATGTATGATTGTTTATTATATATATGCCATAAACATTTCTTA 228
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                                                                                      32 UUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUCUUAAUAAUUAGGUUAACUAUUUUAGUU 91
92 UUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAUAUCCAGGACACCCUCUCUGCUUCUU 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 UUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUCUUAAUAAUUAGGUUAACUAUUUAGUU 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
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28.2%;
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                                                                                                                                         Score 36; DB
Pred. No. 39;
34; Mismatches
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                                                                                                                                                                                 8; Length 142947;
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                                                                                                                                                                                                     GENERAL INFORMATION
APPLICANT: BROWN,
APPLICANT: FORMAN
APPLICANT: DENDY,
                                                                                                                                                                                                                                                                                 Sequence 87, Application US/10345072 Publication No. US20030237112A1
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             FILE REFERENCE: 16313-0210
CURRENT APPLICATION NUMBER: US/10/345,072
CURRENT FILING DATE: 2003-01-16
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APPLICANT: FORMAL
APPLICANT: DENDY
                                                                      TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE TITLE OF INVENTION: PLANTS
                                                                                                              APPLICANT:
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ORGANISM: Raphanus sativum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: JIN, HUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 18.5%; Score 35; DB Local Similarity 37.3%; Pred. No. 97;
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                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                              LAI, FANG MING
LEFOREST, MARTIN
                                                                                                                                                                   DENDY, CHARLES
LANDRY, BENOIT S.
CHEUNG, WING
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CATION NUMBER: PCT/US02/22217
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RESULT 15
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                                                                   Sequence 1, Application US/10312841 Publication No. US20030186277A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 108
LENGTH: 37184
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TYPE: DNA
ORGANISM: Raphanus sativum
FEATURE:
NAMES/KEY: modified base
LOCATION: (144241) . (144300)
OTHER INFORMATION: a, t, c, g
                                                                                                                                                                                                                                                                                                                                                                              Query Match
APPLICANT: Epigenomics AG TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb FILE REFERENCE: E01/1208/WO CURRENT APPLICATION NUMBER: US/10/312,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Epigenomics AG TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
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PRIOR APPLICATION NUMBER: 60/305,026
PRIOR FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/308,736 PRIOR FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/305,363 FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                       19 UUCCUUAUACAAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUCUUAAUAAUUAGGU 78
                                                                                                                                                                                                                                76 GGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAG 117
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Similarity 37.3%;
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o. US20040142334A1
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                                                             Sequence 25522, A Sequence 53, Appl A Sequence 511, Appl Sequence 51890, A Sequence 51890, A Sequence 13374, A Sequence 13374, A Sequence 47663, A Sequence 47663, A Sequence 203, Appl Sequence 203, Appl Sequence 33762, A Sequence 33762, A Sequence 33782, A Sequence 39438, A Sequence 3643, Appl Sequence 3644, Appl Sequence 36
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| 1256 | 201 | 201 | 2988 | 1625 | 1512 | 1222 | 3758 | 3285 | 3021 | 2760 | 2132 | 1894 | 1357 | 1239 | 1173 | 309 | 309 | 159138 | 7785 | 2051 | 193789 |
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| Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | sequence |
| 35396, | 22013, | 18111, | 47496, | 31674, | 42903, | 55775, | | 3728, Ap | 4315, A | 52376, A | 398, App | 4364, Ap | 45763, A | 367, App | 1421, A | 1407, Ap | 357, Ap | 13230, | 65, Appl | w | TOOM 'CC |

ALIGNMENTS

US-10-750-185-25522 US-10-750-185-25522 Sequence 25522, Application US/10750185 Publication No. US20050260603A1 GENERAL INFORMATION: APPLICANT: MI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: ERRR, Richard APPLICANT: ROSENFELD, David APPLICANT: HOLM, Tom APPLICANT: BATES, Stephen APPLICANT: FANTIN, Dennis TITLE OF INVENTION, COMPOSITIONS FOR INFERRING BOVINE TRAITS FILE REFERENCE: MMI1100-2 CUURRENT APPLICATION NUMBER: US/10/750,185 CUURRENT APPLICATION NUMBER: US 60/437,482 PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31 NUMBER OF SEQ ID NOS: 64922 SOFTWARE: PATENTIN VERBION 3.1 SEQ ID NO 25522 LENGTH: 994 "TYPE: Number: Number: US/10/750,185 S 밁 Ś ; TYPE: DNA ; ORGANISM: Bovine 19866881820768 US-10-750-185-25522 Matches Query Match Query Match 18.6%; Score 35.2; DB 6; Best Local Similarity 27.7%; Pred. No. 0.42; Matches 31; Conservative 33; Mismatches 48; 615 AGCAGGACTGTCTCATCATTGTGTTGCTTATTTTATTCCCAGTCTGTTTACCTCCTG 675 TCAGCCTGATGGTGCGCCTGCTTACCTGTCTTGTTTTTAATTTATCCCTTTG 726 54 АGUAGUGCUAUCUUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUG 113 48; Indels 0; Length 994;

RESULT 2 US-10-750-185-54894/c

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Sequence 54894, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.

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; ORGANISM: Bovine 19866880677518
US-10-750-185-54894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/11121086
publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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                                                                                               99264 AACTTTAAATAATTAAGGTATTTATATATTCTCATAGT 99227
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                                                                                                                                                                           GCTATTCTGCGATACGGTTTATACATATAGTTTTGCATGCTTAAAAAGGAATGAAGATAAG 99265
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27.9%; Pred. No. 2;
Live 34; Mismatches
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RESULT 6
US-10-750-185-51890/c
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US-10-995-561-65122
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65122
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65122, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
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GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
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CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR PELICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
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                                                                                                                            112 ATATGATTTTAYCTGTTTCTTCTTACCTTTTAATATGGCTACTAGAAGCTCTAAAAT 56
                                                                                                                                                                                                                     172 TAATTTCTTATATTCATCACACATTGAAAGGATAATATCTTAGACATTGGATTAAAGAAA 113
                                                                                                                                                                 70 UAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAU 126
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                                                                                                                                                                                                                                                                                                                 17.0%; Score 32.2; Dilarity 30.8%; Pred. No. 1.9; Conservative 28; Mismatches
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-995-561-13374
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; ORGANISM: Bovine
US-10-750-185-51890
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Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 13374
LENGTH: 66916
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SEQ ID NO 51890
LENGTH: 1358
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                                                                                                                                               Query Match
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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APPLICANT: DENISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                        Match 17.0%;
Local Similarity 30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 UUAUACAAUUUUGAGAGGUUAAUAAGAAGGAAGUAGUGCUAUCUUAAUAAUUAGGUUAAC 82
 70 UAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUAAU 126
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                                      TAATTTCTTATATTCATCACACATTGAAAAGGATAATATCTTAGACATTGGATTAAAGAAA 51693
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                                                                                                            Conservative
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28.7%; Pred. No. 3.3;
                                                                                                        ; Score 32.2; DI
; Pred. No. 9.4;
28; Mismatches
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                                                                                                                                             DB 6; Length 66916;
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US-10-750-185-26975
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Matches
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APPLICANT:
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     LENGTH: 3000
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; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Bovine 19866880882569
US-10-750-185-34293
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34293, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
SOFTWARE: PatentIN version 3.1 SEQ ID NO 26975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26975, Application US/10750185 Publication No. US20050260603A1
                                                APPLICANT: HOLM, TOM
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIOD-2
CURRENT EPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
CHORENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MMI GENOMICS, 1
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      966 TAAATTAGTGAAATCTGAATATGTATTACAAAAGTACAAGATTATTATTTCCAGTGACAT 1025
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                                                                                                                                                                                                                                                                                                                           ROSENFELD, David
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KERR, Richard
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; ORGANISM: Bovine
US-10-750-185-47663
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US-10-750-185-47663/c
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Publication No. US20050260603A1
GENERAL INFORMATION:
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SEQ ID NO 47663
LENGTH: 3824
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                  APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                     APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KOSENFELD, David
APPLICANT: HOLM, Tom
PRIOR APPLICATION NUMBER: US 60/437,482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 32.7%; Pred. No. 5.2; es 35; Conservative 25, Minmath
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 CUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAAUAACCU 189
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36.1%; Pred. No. 5.6;
tive 21; Mismatches
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US-11-117-187-203
Sequence 203, Application US/11117187
Publication No. US20050266560A1
GENERAL INFORMATION:
APPLICANT: PREUS, DAPHNE
APPLICANT: PREUS, DAPHNE
APPLICANT: OF INVENTION: PLANT ARTIFICIAL
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMILIO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT ELING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
NUMBER OF SEQ ID NOS: 64922
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; ORGANISM: Bovine
US-10-750-185-47569
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Publication No. US20050260603A1
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NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 47569
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APPLICANT:
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ORGANISM: Bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 ССАССАСАСССИСИСИИСИИАИАИСАИИАССИИСИИИИАСАЛИЛАСАЛАЛА 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS

FILE REFERENCE: ARCD: 309US

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RESULT 14

US-10-793-626-1161/c

Sequence 1161, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

PILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PAGENTIN Ver. 2.1

SEQ ID NO 1161

LENGTH: 321
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US-10-750-185-33762
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; TYPE: DNA
; ORGANIZSM: Arabidopsis thaliana
US-11-117-187-203
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Sequence 33762, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: CERN, Richard
APPLICANT: KOSENFELD, David
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CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 30.6; DB 6; Length 321; 32.3%; Pred. No. 6.2; ive 24; Mismatches 39; Indels
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Search completed: December 22, 2005, 16:41:03 Job time : 175.462 secs
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; ORGANISM: Bovine 19866880800866
US-10-750-185-33762
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Tocal Similarity
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SEQ ID NO 33762
LENGTH: 2170
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                     262 GÁAATTÁTTTATTATAGTÁCTCÁCTTGTGÁGGATCTTTTÁÁGÁGACÁTACÁGTCTTÁTA 321
                                                                          322 TTCATTTTAGGATATCTAATTGTATTCAGTTTTAGGCATGTATTTTAG 370
                                                                                                               66 UUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGG 114
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          December 22, 2005, 04:46:32 ; Search time 1483.08 Seconds (without alignments) 7205.664 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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188
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SUMMARIES

| 18 | c 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | U | 4 | u | N | _L | Result |
|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-----------------------|
| 40.8 | 42.6 | 42.6 | 46.4 | 46.4 | 46.4 | 46.4 | 63.4 | 63.4 | 63.4 | 123.6 | 123.6 | 123.6 | 125.2 | 125.2 | 188 | 188 | 188 | Score |
| 21.7 | 22.7 | 22.7 | 24.7 | 24.7 | 24.7 | 24.7 | 33.7 | 33.7 | 33.7 | 65.7 | 65.7 | 65.7 | 66.6 | 66.6 | 100.0 | 100.0 | 100.0 | Query Match |
| 140570 | 220694 | 184134 | 9275 | 9275 | 187 | 187 | 8550 | 190 | 190 | 9264 | 189 | 189 | 1345 | 1345 | 9185 | 188 | 188 | Query Match Length |
| 14 | 14 | 14 | 13 | 13 | σ | σ | 13 | σ | σ | 13 | σ | σ | σ | σ | 13 | σ | σ | BB |
| AC132079 | AC155178 | AC151155 | AB183472 | AB017037 | BD177016 | BD173512 | AF183905 | BD177020 | BD173516 | AF014388 | BD177017 | BD173513 | AR511394 | AR496112 | AF218039 | BD177018 | BD173514 | ĬĎ |
| AC132079 Felis cat | AC155178 Bos tauru | AC151155 Bos tauru | AB183472 Himetobi | AB017037 Himetobi | BD177016 Novel tra | BD173512 Novel ter | AF183905 Black que | BD177020 Novel tra | BD173516 Novel ter | AF014388 Drosophil | BD177017 Novel tra | BD173513 Novel ter | AR511394 Sequence | AR496112 Sequence | AF218039 Cricket p | BD177018 Novel tra | BD173514 Novel ter | Description |

| 44 | c 43 | 42 | 41 | 40 | 39 | | | c 36 | 35 | 34 | c 33 | 32 | c 31 | 30 | c 29 | 28 | 27 | c 26 | 25 | 24 | | | c 21 | c 20 | 19 |
|---------------------------|--------------------|--------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 37.4 | 37.4 | 37.4 | 37.4 | 37.4 | 37.4 | • | 37.8 | 37.8 | 38.2 | 38.2 | • | 38.6 | 38.6 | 38.6 | 38.6 | 38.6 | 39.6 | 39.6 | 39.6 | 39.6 | 40 | 40 | 40 | 40.6 | 40.8 |
| 19.9 190024 | 19.9 166777 | 19.9 69248 | 19.9 5504 | 19.9 5504 | 19.9 5504 | 20.1 251750 | 20.1 228760 | 20.1 226138 | 20.3 9829 | 20.3 9812 | 20.4 194464 | 20.5 181150 | 20.5 179216 | 20.5 70185 | 20.5 53711 | 20.5 221 | 21.1 226020 | 21.1 190904 | 21.1 160624 | 21.1 156604 | 21.3 215706 | 21.3 178377 | 21.3 130263 | 21.6 118765 | 21.7 141299 |
| 14 AC025336 8 AC122714 | | 8 AC113427 | 6 AX349003 | 6 AX344346 | 6 AX251954 | 14 AC097029 | 14 AC149728 | 14 AC103252 | 6 AX763949 | 13 AF536531 | 14 AC160270 | 8 AC007256 | 14 AC074016 | 14 AC091168 | 8 AB038985 | 8 HS197H11R | 14 AC087689 | 8 AP002358 | 14 AC144418 | 14 AC069371 | 14 AC166192 | 14 AC166593 | 8 HS681N20 | 5 BX649275 | 14 AC132080 |
| AC122714 Homo sapi | AC106813 Homo sapi | AC113427 Homo sapi | AX349003 Sequence | AX344346 Sequence | AX251954 Sequence | AC097029 Rattus no | AC149728 Bos tauru | AC103252 Rattus no | AX763949 Sequence | AF536531 Aphid let | AC160270 Bos tauru | AC007256 Homo sapi | AC074016 Homo sapi | AC091168 Homo sapi | AB038985 Homo sapi | Z65084 H.sapiens C | AC087689 Homo sapi | AP002358 Homo sapi | AC144418 Rattus no | AC069371 Homo sapi | AC166192 Pongo pyg | AC166593 Pan trogl | AL031670 Human DNA | BX649275 Zebrafish | AC132080 Felis cat |

ALIGNMENTS

| Query Match Best Local | ORIGIN | FEATURES source | | JOURNAL | REFERENCE AUTHORS TITLE | ACCESSION VERSION KEYWORDS SOURCE | RESULT 1 BD173514 LOCUS DEFINITION |
|---|--|---|--|---------|--|--|---|
| Match 100.0%; Score 188; DB 6; Length 188; Local Similarity 66.5%; Pred. No. 6.4e-38; | /organism="Cricket paralysis virus" /mol_type="genomic RNA" /db_xref="taxon:12136" | FH Key Location/Qualifiers FT source 1188 FT Location/Qualifiers Location/Qualifiers 1188 | PD 08-AUG-2002 PD 08-AUG-2002 PP 31-JAN-2001 WO 2001JP000641 PR 25-JAN-2001 JP 01P 016746 PI NOBUTIKO NAKASHIMA, YASUSHI KANAMORI PC C12N15/11,C12N15/86,C12P21/02 PC Novel tertiary structure having ability to accelerate CC translation activity | RES | Viruses; BaRAN positive-strand viruses, no DNA stage; Dicistroviridae; Cripavirus. 1 (bases 1 to 188) Nakashima, N. and Kanamori, Y. Novel tertiary structure having ability to accelerate translation | | BD173514 188 bp RNA linear PAT 18-FEB-2003 Novel tertiary structure having ability to accelerate translation |

VRL 02-JUL-2000

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BD177018
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OS Cricket paralysis v....

OS Cricket paralysis v....

SS Cricket paralysis v....

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SS Cricket paralysis v....

PN JP 2002306168-A/4

PD 22-OCT-2002

PP 25-JAN-2001 JP 2001016746

PI NOBUHIKO NAKASHIMA, YASUUSHI KANAMORI

PC C12N15/09,C12N1/15,C12N1/10,C12N15/00,C12R1:92) CC

(C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC

(C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC

NOVEL translational activity-promoting higher-order structure FH

Location/Qualifiers

1. 188

1. 188

1. 771 sm='Cricket paralysis virus'.
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       181
                                                                          121
                                                                                                   121 ACAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUUAAGAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125;
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Nakashima, N. and Kanamori, Y.

Novel translational activity-promoting higher-order structure

Patent: JP 2002306168-A 4 22-OCT-2002;

DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND

ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION

ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
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JP 2002306168-A/4.
Cricket paralysis virus
Cricket paralysis virus
Cricket paralysis virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
1 (bases 1 to 188)
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Novel translational activity-promoting higher-order structure.
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       AUUUACCU 188
                                                               CAAAAAUGUGAUCUUGCUUGUAAAAUACAAUUUUUGAGAGGGUUAAUAAAUUACAAGUAGUGC
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/mol_type="genomic RNA"
/db_xref="taxon:12136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 188; DB 6; Length 188; 66.5%; Pred. No. 6.4e-38; tive 63; Mismatches 0; Indels
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181 ATTTACCT 188
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Wilson, J.E., Powell, M.J., Hoover, S.E. and Sarnow, P.
Naturally occurring dicistronic cricket paralysis virus RNA is regulated by two internal ribosome entry sites
Mol. Cell. Biol. 20 (14), 4990-4999 (2000)
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University, 299 Campus Drive, Stanford, CA 94305, USA
Location/Qualifiers
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
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/ (LTAINS LATIONATINNIATINNIMSLEELAAQELIAAQEGILDGFFCTFYVO 
SKROLLDLESECYCMDDEDCGCDR | KREBELRKLI FITSDVYGYNFEEWKGLIWKFVO 
SKROLLDLESECYCMDDEDCGCDR | KREBELRKLI FITSDVYGYNFEEWKGLIWKFVO 
NYCPEHRYGSTFGNGLLI VS PR FYMDHLDWFQOWKLYSSNDECKAFILKRATQLLMSGD 
VESNEGPYGSRPYACDNDRA RIFLEKALQREDEKISTLIKKLRQEI KNNR YTYGGFF 
DDLKGAKGEVGGLMGNLTRI COPLENGLFTTAQI QTTVLTTDKYVNLKEDLLKVAI 
LLVILVRLLMVWKKYRAALI VI I I FYMHFYGFDKQI LD I TVLTTDKYVNLKEDLLKVAI 
LLVILVRLLMVWKKYRAALI VI I I FYMHFYGFDKQI LD I TVLTTDKYTLKKELQEFT 
EEVYHPWFDTCGKLI FRANLAFPAI KKI PGKODWDNYI SRLDRI FKALEGSKKI VDYC 
SEYFNLSVDEVKKYVLGKELKGTQGLYDE I HWAKEI RHYLDL DERNKI TLDTETAAK 
VEDLYKKGLKYSEEKI PDRDI ARFITTMLF FAKSI YEQVILS PVKGGGFROMF PI TVML 
TGSGGIGKTQMI YEYLCI DI LRENGI VREDAYKHQAYARQVETEYWDGYNGGKY VI YDD 
AFOLKDDKYKSWEDI FEVIRTCNTF PQHLHMAALQDKNMYSQAEVLL YTTNOFOVQLE 
SITFPDAFYNRMKTHAYRVQI KQEKSI WRNAAGEEXYALDVTCLNKUEA I DLSVYEF 
QXMRFDDDSATKWI DDGSPI SYDBFARTI CKAWKEEKEKTFHOLQWLEAYASRTVAQG 
GSETSKYYDWDETYFSNILLSQGFMAGKSLI IEMEAEFASDAETFNAYI EYKKNI PKET 
KMSKMTILDEQI SALSTKI RELKNKAYKI I SEHPYLTALGFI CVMI SAFAMYSFER 
TLIDDTITSEVGSSGDNKTQKLSKRV VENVGGSGDVKTTKAKFYARSON 
KITKVENGSSGDSKTOKA 
KITKVENGSSGDSKTOKA 
KITKVENGSGDSKTOKA 
KITKVENGSSGDSKTOKA 
KITKVENGSCHEREKATHOLGEI TI YHEDTDMFDYESESYT 
QROLTENGAKRYKLATATFLROWCHMPYHF I ETLYAKVABSTNI YESQPNCDDVI 
VVPVSHFLAPNAREVELITACTRI HYKDGETPEGKECALGKSNI KYGQAVETTLLK 
SCIYGMLSKPI TKPAHLITRTRL PNGE I VDLAKGLKKGVDTAVLDAEI VESAALDVK 
QVVLTQYNSMLDVNKYRRFLT YEBAFTACHSTON 
QVTLTQYNSMLDVNKYRRFLT YEBAFT COTGDDDFMKGLKGCYDTAVLDAEI VESAALDVK 
QVTLTQYNSMLDVNKYRRFLT YEBAFT COTGDDDFMKGLKGCYNDTAVLDAEI VESAALDVK 
QVTLTQYNSMLDVNKYRRFLT YEBAFT COTGDDDFMKGLKGCYNDTAVLDAEI VESAALDVK 
QVTLTQYNSMLDVNKYRRFLT YEBAFT COTGDDDFMKGLKGCYNDTAVLDAEI YERAYDAG.
                                                                                                                                                        HSVHSYGDNVYMWTHSQPSGNPFTVIINCLYNSMIMRIVWILLARKLAPEMQSMKKFR
ENVSMISYGDDNCLNISDRVVEWFNQITISEQMKEIKHEYTDEGKTGDMVKFPSLSEI
HFLKKRFVFSHQLQRTVAPLQKDVIYEMLNWTRNTIDPNEILMMNINTAFREIVYHGK
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KTRVFSAGFQHFVVAFRKYFLPFAAYLMNNRIDNEIAVGTNVYSTDWERIAKRLKKHG
NKVIAGDFGNFDGSLVAQFFGQSCGKSFYPWFKTFNDVNTEDGKRNLMICIGLWTHIV
                                                            codon start=1
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/db_xref="taxon:12136"
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/protein_id="AAF80998.1"
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AUTHORS
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AR496112
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JOURNAL
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Best Local
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1 (bases 1 to 1345)

1 (bases 1 to 1
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                                        UUUUUGUAUUUAGGUUAGCUAUUUAGGUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCAC 122
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EMDLSRVLSIENYWDRFTWKTSDVTNITVLWDDXYVSPFKVKFSATITDRFRCTHMGYV
ANAFTYWRGSIVYTFKFVKTQYISGRLRISFIPYYNNTISTGTPDVSRTQXIVVDLR
TSTEUSFTVPYLASRPWLYCIR PESSWLSKDNKDGALMYNCUSGIVRUSVLNQLVAAQ
NVFSEIDVICEVSGGPDLEFAGPTCPSYVPYAGDLTLADTRKIEAERTQEYSNNEDNR
ITTQCSRIVAGVMGEDQQIFRNEAQHGYHPISIDTHRISNNWSPQAMCIGEKIVSIRQ
LIKRFGIFGDANTLQADGSSFVVAPFTVTSFTKLTSTRNUTQDFYYYLAFWRGSN
RIKMVAETQDGTGTFRKKTNFTWFVRHNSLQDSFNSLISTSSSAVTTTVLPSGTINM
GPSTQVIDPTUEGLIEVEVFYNISHTFAVTIDGTPSMEDYLKGHSPPCLLTFSPR
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VNLSTMYLDMTTREDRIHSIKDFLSGPIIIATMLMSSSDPVEKOLYTANFPEVLISNA 
MYQDKLKGFVGLRATLVYKVQVNSQPFQOGRLHQYIFYAQYMPNRVTLINETLQGRS 
GCPTTDLELSYGTEVEMRIPYVSPHLYYNLITQGGSFGSIYVVVSQLHDQVSGTGSI 
EYTVMAHLEDVDVQYPTGANIFTGNSPNYLSIAERIATGDFTETEMRKLMIHKTYLKR 
PARIYAQAAKELKQLETNNSPSTALGQISEGLTTLSHIPVLGNIFSTPAMISAKAADL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="unknown"
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                                                                                                                                                                                                                                                                            66.6%; Score 125.2; DB 6; 51.1%; Pred. No. 7e-22; rative 53; Mismatches 38;
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Pred. No. 3.4e-38;
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at US
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Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L., Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R. Drosophila sequences
Patent: US 6703491-A 16354 09-MAR-2004;
Exelixis, Inc.; South San Francisco, CA
Exelixis, Inc.; South San Francisco, CA
1. .1345
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Sequence 16354 from patent US
AR511394
PATENT: WO 02061080-A 3 08-AUG-2002;
JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE SERICULTURAL AND ENTOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
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(bases 1 to 189)
Nakashima, N. and Kanamori, Y.
Novel tertiary structure having ability
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WO 02061080-A/3.
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PF 25-Ja
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B0177017.1 GI:30014277
JP 2002306168-A/3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dicistroviridae; Cripavirus.

1 (bases 1 to 189)

Nakashima, N. and Kanamori Y.

Novel translational activity-promoting higher-order structure Patent: JP 2002306168-A 3 22-0CT-2002;

DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
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                                                                                                                                                                                        PF 25-JAN-2001 JP 2001016746

PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02// PC

(C12N15/09, C12R1:92), C12N15/00, C12N5/00, (C12N15/00, C12R1:92) CC

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(C12N15/09, C12N1:92), C12N1:92)

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JP 2002306168-A/3
22-OCT-2002
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illarity 51.1%;
Conservative 5;
                                                                                                                                                                                source
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31-JAN-2001 WO 2001JP000641
25-JAN-2001 JP 01P 016746
NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
C12N15/11, C12N15/86, C12P21/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     017 189 bp RNA linear PAT 16-APF
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WO 02061080-A/3
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                                                                                             /organism='Drosophila C
                          /organism="Drosophila C virus
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/mol_type="genomic RNA"
/db_xref="taxon:64279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
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Pred. No. 2.5e
52; Mismatches
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                                                                                                                                       virus'.
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 UUACCU 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 TAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 TCTTAATAATTAAGTTAACTATTTAGTTTTACTGTTCAGGATGCCCTATTGGCAGCCCCAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; saRNA positive-strand viruses, no DNA solicistroviridae; Cripavirus.

1 (bases 1 to 9264)
Johnson, K.N. and Christian, P.D.
The novel genome organization of the insect pictorosphila C virus suggests this virus belongs to the contract of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-1997) Entomology, Canberra, ACT 2602, Australia
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Johnson, K.N. and Christian, P.D.
Direct Submission
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J. Gen. Virol. 79 (Pt 1), 191-203
9460942
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Drosophila C virus
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="replicase polyprotein"
/protein_id="AAC58807.1"
/db_xref="GI:2388673"
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/mol_type="genomic RNA"
/strain="EB"
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/db_xref="taxon:64279"
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NSEYGDCIDFVDDIAKRLQKGETLEEIBFDYASDPEMFTQYYHFKSTIKPASRWQKYK

HRMSAFNNMTDEEFDNCTYEDLNKDQKRELAQWSTKDSWLGRFFLSRDRKNKVGIWAE

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RESULT 9
BD173516
LOCUS
DEFINITION
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VERSION
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   173516.1 GI:28414847
02061080-A/6.
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/protein | da"AAC58808.1"
/protein | da"AAC58808.1"
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/db_xref="GI:2386674"
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WTHSQPSGNPFTVIINCLYNSIIMRLSWIRVWEKFQPRLKSMKWFNEYVALITYGDDN
VLNIDAKVVEWFNQINISEVMTEMRHEYTDEAKTGDIVKSRKLEDIFFLKRKFRFSPE
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TRTGDGSIIGLYNKYLERKIIGMHIAGNDAEBHGYACPLTQECLETAFSALVNKNKK
NISSOFYYEIFUMVDPLGDSSVPEGKRYALGKSSIRVGQAVNSSIIFSRIYGKLSVPT
MKPALLKPTILNNKVHNPLLSGLKKCGVDTAVLSDDEVLSASQDVCRVMLNQYNKNLN
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TSNYALLAKROVQGLIEDCASKKISNVIFVOTLKDERRDIAKVNVGKTRPVESACPQHF
VYAFRQYFLPFAAMLMHNRISNEVAVGTNVYSSDWERIAKRLKTKGSHVIAGDPGNFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRFKLQAVRTNSAETSVKTDTTWTVNLWNSVQDSFNSLINVFSTTDYPIKSTGALPAG
TSGFGNSMTYIDPEVEGFMEFEIPYYNISHISPATTYVRGTESPITINSVLRGHLPPQ
IVAVAPQGTIATTDVVNAQFARAPSDDFSFMYLVGVPPLTNVARP"
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DKRYQLGNCTFVRGWSFIMFYHFVQAVFARRLFPNTIISLSQQWSEDLMQIFLSHFFS
AGVDNFYLTDNCVRLFFKNGDFRDCVMVNLHSRWCTFHRDLVRHFILTSDQGKLKGSF
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51.1%;
                                                                                                                                        structure
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Pred. No. 1.3e-21;
                                                                                                                                    190 bp
having
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                                                                                                                                        to accelerate translation
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BD177020
LOCUS
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                                                                    unclassite.

(bases 1 to 190)

Nakashima, N. and Kanamori, Y.

Novel translational activity-promoting higher-order structure
Patent: JP 2002306168-A 6 22-CCT-2002;

DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND
ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION
ENTOMOLOGICAL GENERAL OF AGRICULTURE FORESTRY AND
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FISHERIES
OS Black
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Novel trans
BD177020
BD177020.1
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JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF
SERICULTURAL AND ENTOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE
FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
                                                                                                                                                                                                                                              unidentified
                                                                                                                                                                                                                                                                unidentified
                                                                                                                                                                                                                                                                                   JP 2002306168-A/6.
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Nakashima, N. and Kanamori, Y.
Novel tertiary structure having ability to accelerate translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACAATGTGATCTTGCTTGCGGAGGCAAAATTTGCACAGTATAAAATCTGCAAGTAGTG
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                 Black queen-cell virus
JP 2002306168-A/6
22-OCT-2002
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25-JAN-2001 JP 01P 016746
NOBUHIKO NAKASHMA, YASUSHI KANAMORI
C12N15/11,C12N15/86,C12P21/02
Novel tertiary structure having ability
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 25-JAN-2001 JP 2001016746
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WO 02061080-A/6
                                                                                                                                                                                                                                                                                                                                    020 190 bp RNA linear PAT 16-APR translational activity-promoting higher-order structure.
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/mol_type="genomic RNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                   GI:30014280
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AF183905
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VERSION
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Black queen cell virus
Viruses, ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8550 bp ss-RNA linear VRL 16-AUG-2000 Black queen cell virus nonstructural polyprotein (orf1) and structural polyprotein (orf2) genes, complete cds. AF183905
                                                                                                                                                                                                                                                                    Submitted (06-SEP-1999) Microbiology, University of Western Cape, Modderdam Rd., Cape Town, Western Cape 7535, South Africa Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        Leat, N., Ball, B., Govan, V. and Davison, S. Analysis of the complete genome sequence of a picorna-like virus of honey bees
J. Gen. Virol. 81 (Pt 8), 2111-2119 (2000)
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CC12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02// PC
(C12N15/09,C12N1/90,C12N1/90,C12N15/00,C12N1:92) CC
(C12N15/09,C12N1:92),C12N15/00,C12N1:92) CC
Novel translational activity-promoting higher-order structure FH
Key
Location/Qualifiers
FT Source
1 190
forganism='Black queen-cell virus'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTATCAATATCTAGGAGAACTGTGCTATGTTTAGAAGATTAGGTAGTCTCTAAACAGAAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATTGTTGGAATCACCGTACCTATTTAGGTTTACGCTCCAAGATCGGTGGATAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 8550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 8550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
/codon_start=1
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/strain="South African"
/specific host="Apis mellifera"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unidentified"
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism='Black queen-cell virus'
                                                                        gene="orf1"
                                                                                                               gene="orf1"
                                                                                                                                                                                                                                                        . 8550
                                                                                               . 5625
                                                                                                                                     .5625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.7%;
42.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                      8),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63.4; DB 6;
Pred. No. 7.9e-06;
3; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              black
                                                                                                                                                                                                                                                                                                                                                                                                                                              queen-cell virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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5

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밁 Ş 밁

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/gene="orf2"
5834. .8395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_except=(pos:5834...5836, aa:Met)
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/protein id="AAF72338.1"
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CDIAKETEVSLRIFFYSPYNSYDLVSKAFPMAKVUGLVYSPLTTIPTVLTVGTUKGEHLP
FLKSGAMWVSENILQPADEIIGPILSLFGFSKPLLPTINFTVLRAAFKQSVSKLGEHLP
FLKSGAMWVSENILQPADEIIGPILSLFGFSKPLLPTINFTVLRAAFKQSVSKLGEHLP
FLKSGAMWVSENILQPADEIIGPILSLFGFSKPLLPTINFTVLRAAFKQSVSKLGEHLP
                                                                                                                                                           HSLALSNDTNVPFVKALDGSGLDEMSFDYLKKI PQFIQSKFFTTTTKPQEVLFQTKVM
PHYFVPAGDVTVAMDKDKTRT I WQPSHLAYI TSMFKYWTGSLVYFFKFVYKTDYHSGRV
EISFHPFSDYTANSYSDYTYRI I VDLREKSEFSVTI PFISPVPYKRI SRPDWDKPYSK
YAHASTGTLVLKALTSLKATIVTVVSNSVEILI EVNAGDDFNVI APIENI FPFFSLSPG
RKGMVAQSNSGTEQQNPRGSSLLTDPESI TKSDPYNPNI SLLI SGEVFTNFRNLI KRV
NFRKATTLNGKR I SDTFDINSLI EAPRLDI AQYVDTETKEAKYGFSYFWSAPTTLNI V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIMIKKTVNYVKVTLLCHDPBEELENGSDPLVDWEEQCRKHFVSDTDRIAIYTESTLA
DIKRLYNMGVSYMRHPLYKFHQRVISEILNQLLRFADKIKKKYGTDASVRNPEVTLYL
YGETGVGKSTLTYPLCATLLKTIFTREGNTVMLESILKQHYKEMIYVRAAEQEFWDGYT
QQLYTVEDDFNQQVDSSANPSLELFEIIRSSNIFPYPLHMASIEEKANTYCGSKVILV
GSNNKTPKTESLNYPKALLRRFAKFVEVKRAPSESGTFSTDCYTFVEYDPFDHCNIVK
SSNNKTPKTESLNYPKALLRRFAKFVEVKRAPSESGTFSTDCYTFVEYDPFDHCNIVK
SNSYNELIDEVVAMYFHEGEFVSSVDKFIMENVFAQGGSLSDSEDDFIEASSYGDSN
LDEALTREEKKEIIECINDQFKMENDTRTSFQLIRDYFHCAKDSLQBKFLAVRRKYSE
DDWFSFSKASKVVLGILSLVLVGYGIYSYVKGNPAKDSAESYEBKVASKAKVEGSNGV
PEAYESKVNRKLNVEGYNARDLKRKYEAYAFKVRFTVESSEVITHVNSLIEKGDDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPFVICEGWTPAKI FGNGDEYDMSTSGVQMLREKVQECI EAARQGKI LDHYFI DTLKDE
RKPKHKAHKSRMFSNGPI DYLWSKMY FUD I DAVLSELKOVDH IS VGSNYYSTDMDVI
ARYLKSKSHHIVAGDFEGFDASEQSDI LYAAGBVLQELKKI FYSTEDEMLQQRAI II
SLVNSLHI NENGI VLQWCKSLPSGHYLTAI I NSVFVNLVMCLVFMEANQKYSFTTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCFATPFYLEDVKEILSRYDYKAQSCAFELVLRQDLEPCALPNHLDECEFILMGKVKD
PPVQPSRSKISPSPLYGHITEPSSAPTWLYPRELDGQIFDPLKYRTARLGKDSVPIRS
KLINLAKMALIDDIYSVYLQKKDLLDGRFPSSLTFDQAVLGIPGEDYVNSIKRDTSCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRAYELDDGAILQFNHPYGKRNFFTFIGDIQFSLYKTKNISKTNDLDSRDLMHFVVDK
SVVHRDISSYFCERLELQSVGSTRIQLPVMRWVRDVGYIFVKSGQGTSCIKNVSNVSY
MTDTDPDAREIRLRBAWEYSLETISGDCGAPLFVTNSKIGPGKIIGIHTAGGHRFGVG
                                                   AEMYALYRGGVRVKVVTEKGVDFVRATVSPQQTYGSDVAPTTHISTPLAIEQIPIKGV
AEFQIPYYAPCLSSSFRANSETFYYSSGRNNLDIATSPPTVNRYYAVGAGDDMDFSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inde="capsid polyprotein; translation initiation most likely facilitated by an internal ribosome entry site (IRES); a region similar to Plautia stali intestine virus IRES was identified immediately upstream of orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FFRECGIVAYGDDHVVSVPEKYLSVFNQQTLFVLMSKFGMFYTIETKDDTEIDFLSRR
LEDVSYLKRNFVYDESRQRYIAPLSLDVVLEMPMWTKSSKDIVTNVFCNLEHALKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQSEACSDINASEQLTAVTTNNTYVMTILSKESVIRVGHCIFLKGKIAVAPGHYLRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLSYVIPPLFLESVVDTKSNLFKRIWKSKDLDLVVKRLSYFGDAKIYNAFDNIGTWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHDKELWEKWSPVLHSKSEEVLKMVSSLKFQDEVREIALGLSGYE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHELIHTNVAQMNFSIPFSHNLSKDSKAFLTQTVDTSLDGMKQISNETVNTIKEVFET
FLTKMTTTFEQCAEAHCKIKSFCTLFKCSRHFNNVQEAFNFTMSFMRFLALAYAIFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mmepiyentktvtepilyypfrynmnikildltdkegqesvnkk
flrkftklrklclrlqkdtafwkntrsrldmiqddidkmvaqsgpvmsqslsdrvdrm
GTPPCIHASQTAQFTKIKQGKVYDLRYDQYDPFREVQDGTAFLNARSIEDSDLL'
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CDS gene

ORIGIN

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                                                                                        Matches
                                                                                                  Query Match
Best Local :
                                             5648
                       60
                                                      79;
                                                                                                  Similarity
CTATTGTTGGAATCACCGTACCTATTTAGGTTTACGCTCCAAGATCGGTGGATAGCAGCC
                    cuauuuuuuaaauuaacuuaacuuuaacuuuaaceuuccaacaaucccuag-ucccaacc 118
                                            CAACAATGTGATCTTGCTTGCGGAGGCAAAATTTGCACAGTATAAAATCTGCAAGTAGTG
                                                                                        Conservative
                                                                                                33.7%;
                                                                                     43;
                                                                                                  Score 63.4; DB 13;
Pred. No. 4.3e-06;
                                                                                       ed. No. 4.3e-06;
Mismatches 61
                                                                                     61;
                                                                                                          Length 8550;
                                                                                        Indels
                                                                                       2
                                                                                       Gaps
                                             5707
 5767
                                                                  59
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CCACAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAG 178

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RESULT 13
BD177016
LOCUS
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VERSION
KEYWORDS
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BD173512
                             VERSION
KEYWORDS
                                                             ACCESSION
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AUTHORS
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Matches
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 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                              135 A-CCTAGGTGCAGCCTTGTAGTTTTAGTGGACTTTAGGCTAAAGAATTTCAC 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI OS Himetobi P virus

ON Himetobi P virus

NO 02061080-A/2

PN WO 02061080-A/2

PD 08-AUG-2001

PD 08-AUG-2001

PD 09-AUG-2001

PF 31-JAN-2001 WO 2001JP000641

PR 25-JAN-2001 JP 01P 015746

PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

PC C12N15/11,C12N15/86,C12P21/02

CC NOVEL CETTIBY STRUCTURE having ability to accelerate CC
                                                          Novel translational activity-promoting BD177016
                                                                                                                                                                                                                                                                                                                                                                            63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 187)
Nakashima, N. and Kanamori, Y.
Novel tertiary structure having
               Himetobi
                           BD177016.1 GI:30014276
JP 2002306168-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, Dicistroviridae; Cripavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Himetobi P virus
Himetobi P virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BD173512.1 GI:28414843
WO 02061080-A/2.
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                                                                                                                                                                                                             GCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAAACCUAAGAAAUUUAC 186
                                                                                                                                                                                                                                             CTTAGTTATTTAGCTTTACCGCCCAGGATGGGGTGCAGCGTTCCTGCAATATCCAGGGC
                                                                                                                                                                                                                                                                            GGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAA 134
                                                                                                                                                                                                                                                                                                                                            UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATTAGAAGTAAGAAATTCCTAGTTATAATATTTTTAATACTGCTACATTTTTAAGAC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAUU 183
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WO 02061800-A/2
08-AUG-2002
31-JAN-2001 WO 2001JP000641
25-JAN-2001 JP 01P 016746
NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
C12N15/11,C12N15/86,C12P21/02
NOVEL tertiary structure having ability to accelerate
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tertiary structure
P virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO 02061080-A 2 08-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Himetobi P virus"
/mol_type="genomic RNA"
/db_xref="taxon:81583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism='Himetobi
                                                                                                                                                                                                                                                                                                                                                                                          24.7%;
                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                            Score 46.4; DB Pred. No. 0.19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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having
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA
                                                                                                                                                                                                                                                                                                                                                                              71;
                                                                             higher-order
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                                                                              structure.
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                                                                                              PAT 16-APR-2003
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AUTHORS
TITLE
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AB017037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 A-CCTAGGTGCAGCCTTGTAGTTTTAGTGGACTTTAGGCTAAAGAATTTCAC
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                             Direct Submission
Submitted (20-AUG-1998) Nobuhiko Nakashima, National Institute
Submitted (Entomological Science, Department of Insect
Sericultural and Entomological Science, Department of Insect
Physiolosy and Behavior; 1-2 Owashi, Tsukuba, Ibaraki 305-8634,
Japan (E-mail:nakaji@nises.affrc.go.jp, Tel:81-298-38-6109,
Fax:81-298-38-6028)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                            Himetobi P virus
Viruses; ssRNA positive-strand viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PI NOBUHIKO NAKASHIMA,YASUSHI KANAMORI
CC 212N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02// PC
(C12N15/09,C12R1:92),C12N15/00,C12N5/00,C12R1:92) CC
(C12N15/09,C12R1:92),C12N15/00,C12N5/00,C12R1:92) CC
Novel translational activity-promoting higher-order structure FH
Key
Location/Qualifiers
                                                                                                                                                                                                           Nakashima, N., Sasaki, J. and Toriyama, S.
Determining the nucleotide sequence and capsid-coding region of himetobi P virus: a member of a novel group of RNA viruses that
                                                                                                                                                                                                                                                                            Dicistroviridae;
                                                                                                                                                                                                                                                                                                                            Himetobi P virus
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Himetobi P virus genomic RNA,
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Patent: JF 2002306168-A 2 22-07-002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND
ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PR
ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 187)
Nakashima, N. and Kanamori, Y.
                                                                                                                                                                                                                                                                                                                                             nonstructural protein
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                                                                                                                              2 (bases 1 to 9275)
Nakashima, N. and Sasaki, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCUCUCUGCGGUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC 186
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                                                                                                                                                                                               insects
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/mol_type="genomic RNA"
/db_xref="taxon:81583"
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1. .187
             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             precursor;
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 6300 TGATTAGAAGTAAGAAATTCCTAGTTATAATATTTTTTAATACTGCTACATTTTTAAGAC 6359
                           15
                                                   63;
                         UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUA 74
                                                   Conservative
                                                             24.7%; Score 46.4; Di
36.6%; Pred. No. 0.1;
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PVVITUEGGSCVGKSTLTNUKAASILSKIQPDWALKKQGKNLITSRASBQEFWDGYTG
QLUTVFDDBSQRADSAGNPNVELFDIVRAANVYPYPLHAMALSDKASTNETSKIIICS
SNLKQPKTESLNFFNALYRRFDVCVSVSKNEKNDVVDTHFVEDFYQFQEVDMLKKED
LGSTDWEGIVDKCVELYKHRSDEVSSLDEKIQEILQSTQFEDVPLNVAQEQVNCDVLG
FCNCDCWGETMCVMTNLHQPKWKQWLLKWKHVVTGIPKGSVYBAPEKMRFLSQEYLNA
SKSRFGRWLTSIKERFPVIKDLRLIHLVKATVVNGPMVFFGVKKLPAKKNECVELHVS
ESYDVGNIKPTRTESYETPNVKFTKTESYESPNVKSVKTESYESPNVKFVRVEMSFPS
GRVGGSEMALASLQLDNYIKFVKEQGYSDQNAABICSKLVTKNWFKIYVENDHVSIFL
GHVLFIKGRIAIMPHHFLAALKKFKEQHEGGVVFFRNLFLSRAFFVKLEDWIRKVKPF
ESPEPTESLAESFDLGSCCLDNYINFSDVSKLFVSKSDLSYLKSDILLFTLSTENG
QAFAKIKIGRAASGIQRADCRVYGSDPTDRLRLVRXCMFYLEFTLSTENG
QAFAKIKIGRAASGIQRADCRVYGSDPTDRLRLVRXCMCPLROTDEFSFMQYRLEK
FASPCVPVDARMLENGVSAVSNHLCKSILENGLITTSKTKCQLROTDEFSFMQYRLEK
FASPCVPVDARMLENGVSAVSNHLCKSILENGLITTSKTKCQLROTDEFSFMQYRLEK
FASPCVPVDARMLENGVSAVSNHLCKSILENGLITTSKTKFCQLROTDEFSFMQYRLEK
FASPCVPDARMLENGVSAVSNHLCKSILENGLITTSKTKFCQLROTDEFSFMQYRLEK
FASPCVPDARMLENGVSAVSNHLCKSILENGLITTSKTKFCQLROTDEFSFMQYRLEK
FASPCVPDARMLENGVSAVSNHLCKSILENGLITTSKTKFCQLROTDEFSFMQYRLEK
FASPCVPDARMLENGVSAVSNHLCKSILENGLITTSKTKFCQLROTDEFSFMQYRLEK
FASPCVPDARMLENGVSAVSNHLCKSILENGLITTSKTKFCQLROTDEFSFMQYRLEK
FANNTANDARMLENGVSAVSNHLCKSILTTSKTKFCQL
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TRTABITRAIDRI I ALPHVQLDI SBQSEVTLRVPYI SBYSAVALI BGRYRWGRVVVAV
YSPLAQVSQPALKVNI FGYYDAVTLGY PTLGTI ALS PVAVAREQVNLNS EADMLR I AE
SRNFFTKI ASAI INGLI QKGSDILGANULPQTKSFTNPVAKI SDAAFDI I SMI FGFKKPD
KTNHGETVLFR PTQY FGNVDGVEHSHKLGYHAMNRI DFQPDFAGSKMDEMS FDYVKRI
PNYIDSFSYSNSANYGDTLMSTRAVS PCYRSADYTTTNGARNES FPT PTSLTXAI GPFS
LMRGSI VYTFRAVKTEYHSGRI I EFS FNPF INLDMYNTNKTTRS EYVYKVILDLRTQTE
ISFTVPYAGTTPPFKRI REBINPLSSGGI SVDDENVFATGVLGVRALFFLVLGSTVVPS
TIQILVEMKGGPDFEVECPNSTGMMPIHSITPAATGRDTVDSELVSTAQEQANFASTG
OHDIRADYLEDKIEIKDITGI SSNI SLMTEKSILSVOESFGREDLIKR FGRFKNOSV
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FGVNVKKAFEFFEVCGIVAYGDDHIVSVPEWATNVFNQYELASLFKQIGLSYTLEDKD
ATVNAPYRSLNEVSYLKRKFLWDEDKRQYLAPLSLETILETPMWVKKCVDVNLQTTTE
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QQHVFIDTLKDERKPIHKAHKTRMFSACPLDYLIACKMYFGGVVSLLQKSRNICGISV
GTNVYSYDWTIIANTLLSKSPCMIAGDFEGFDSSQLQDILRAASQVLLNVSRDMLGST
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TIFTWIKSTYTMCYRIFSKYVLGVDPGVQVSADSHPVASWLEELGEPYKSFSNGTFSY
DSATFSIIHSLFIRGLNLQRSESFRSDQIAIRTGMDCLNKILTEFRSRNIEAGSVRNP
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FRRKLVMYLLKRCILIESDLPIEIRWKDVCYDERMYEEKIEVQEQVFINVASQSRSDIE
TLYLISMNEVCESMSVERMVAVCECAREQGLFNVSLGINDDTKGYIDSVVSRIGNOVS
LYTDTMLGLEVAASDILVNLKYIVGFLVAAVLVGVATYCGVKMISKLFNFFLSLVFKS
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LKNLNEAIRTTDVFKNYVVELTLGHQDLDFGYFKLYNRDLENLVYSMTSNNETHLHPD
                                                            ĀFTNTKILSGIPIVNYTSSIAGTGLTLTADGGSTPLTMVSSMYAFFRGGFRAKVYIHD
LPAGEMVQGALIDNSQNTNVPQPLALQSLQYELSDKRLYEFSWPYYCPTYLTTYPSGS
LNYISDLVNPTTYARITTISEYATAYAMAAADDFDCGFYLGAPLSWNWEIERLAGRLD
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SSYGFVTSPLRVDPFDKV"
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/db_xref="GI:3493358"
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specific_host="Laodelphax striatellus"
db_xref="taxon:81583"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GGUUAGCUAUUUAGCUUUCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Himetobi P virus
Himetobi P virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB183472 9275 |
Himetobi P virus genomic RNA,
AB183472 AB183472.1 GI:50251148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakashima,N., Kawahara,N., Omura,T. and Noda,H. Spherical viruses isolated from the brown planthopper, Nilaparvata
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Nakashima, N. and Noda, H.
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                                                                                                                      DSATTES I HELF IRCLUIGNDE GYVVSADSHPVASWLEBLGEPYKS FSNGTESY
DSATTES I HELF IRCLUIGNDE GYVVSADSHPVASWLEBLGEPYKS FSNGTESY
DSATTES I HELF IRCLUIGNBESERSDOI AI ETGMDCLIKI LYBERESERSWAP
PVVI Y LHGGSGVGKSTLTNVLAAS I LSKI QPDMNLKKQWKNLI Y SRASEQEFWDGYTG
QLVTVEDDESQRABSAGNPAVELFD I VRAANYY EY PLHMANLSDKASTNETSKI I I CS
SNLKQPKTESLNF PNAL YRRFDVCVSVSKNEKYNDVVPTHFVED FYQFQEYDMLKKED
LGSTDWEGI VSKCVELJYKHRSDFVSSLDEKI OB I LQSTQDEVLNVAQBQVNCDVLG
FCNCDCWGETMCVMTNLHQPKWKQWLLKWKHYVTGI PRGSVYEBAFEKWRE LSQEYLNA
SKSRFGRWLTSI KERFPVI KDLRLI HL VVAT VVMGPMVF FGVKKLFAKKNECVELHVS
SKSRFGRWLTSI KERFPVI KDLRLI HL VVAT VVMGPMVF FGVKKLFVRVEVBSFPS
GRVSGSEMNLASLQLLNY I KEVREQGVEDQNAAE I CSKLVTKNMFKI YVENDHVSI PL
GRVJSGSEMNLASLQLLNY I KEVREQGVEDQNAAE I CSKLVTKNMFKI TVENDHVSI PL
GRVJSGSEMNLASLQLLNY I KEVREQGVEDQNAAE I CSKLVTKNMFKI TVENDHVSI PL
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ESPEPTESLAESRDLCSFCLDNT I NFSDVSKLFVSKSDLSYLKSSDI LL PTLSTPSNG
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ALAGRKIMGIHIAGNTDAGFSTPLYKEDIDTILSMYPLESQVANEQCQPIHMPTGCHL
PESTSFVVLDKIEKPLYASSKSVISPSPLHGILTTPKTKPCQLRDTPEFSPMQYRLEK
FASPCVPVDARMLENSVSAVSNHLCKSILENKDLITTSDKSRYSFEEAVSGIDEEEFI
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LYTDTMLGLEVAASDILVNLKYIVGFLVAAVLVGVATYCGVKMISKLFNFFLSLVFKS
DESMMNVAQEQSSDDTWNGFLMLLMSVFGVSAGALKSARCMNAIRCISMLFRAESGID
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LYMNLBYVMNPNKDLDLLCGENDSWDQYVLSRQLKEMRAIWVGLQAGNVDFILDTVNP
DCQIALYYMTRVLYDAKVCSRRVRRTAYALCRILNHVPEHLMPYINKDLIENFBLCVP
FRRKLVWYLLKRCLLFSDMFLEIRWKDVCYDBRMYEBKIEEVVEGQVFNVASQSRSDIE
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/db_xref="GI:50251149"
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/lab_host="Nilaparvata lugens"
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                                                                        15 UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUA 74
                                                                                                             63;
                                                                                                             Conservative
                                                                                                                                                                                                    /note="translation starts at GCU (alanine) triplet, directed by internal ribosome entry site"
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EEDLLVMQVLLESILSSVHLINNYVYMMLKGLDSGHFITAI INSI FVLISFSSVMQIA
FGVINVKKAFEFFEVGGI VAYGDDH I VSVPEMATINVFNQYELASLFKQJGLSYTLEDDA
ATVNAPYRSLNEVSYLKRKFLMDEDKRQYLAPLSLETVLETPMWVKKCVDVNLQTTTE
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/product="capsid protein precursor"
/protein_id="BAD27585.1"
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                                                                                                                             24.7%; Score 46.4; DB 13; Length 9275; 36.6%; Pred. No. 0.1;
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Search completed: December 22, 2005, 11:33:50 Job time: 1487.51 secs Matches Query Match Best Local Similarity 6420 A-CCTAGGTGCAGCCTTGTAGTTTTAGTGGACTTTAGGCTAAAGAATTTCAC 6470 6360 CCTTAGTTATTTAGCTTTACCGCCCAGGATGGGGTGCAGCGTTCCTGCAATATCCAGGGC 6419 6300 TGATTAGAAGTAAGAAATTCCTAGTTATAATATTTTTAATACTGCTACATTTTTAAGAC 6359 135 GCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC 186

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   number of hits satisfying chosen parameters:
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AAL50545
ABK83573
ACH45871
AAK77216
AAK77217
ADQ97028
ABL60324
ABK31350
ABK10571
AAS61255
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AAL50547
ABZ80709
 ADM47607
ADA20684
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Compugen
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Aal60324 Aphid let
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2 Black que
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14 Rice cDNA
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Cricket p
Drosophil
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The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

a range of

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

Claim 1; Page 33; 39pp; Japanese

WPI; 2003-403230/38.

Nakashima N,

Shibuya

'n

Nishikawa

(WAKE-)

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|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|-------------|--------------------|----------|----------|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|
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| 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.6 | 33.8 | 33.8 | 33.8 | 33.8 | 34.2 | 34.2 | 34.6 | 34.6 | 34.6 | 34.6 | 34.6 | 34.6 | 34.6 | 34.6 | 34.6 | 34.6 | 35.2 | 35.6 | 35.6 | 35.6 |
| 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 17.9 | 18.0 | 18.0 | 18.0 | | 18.2 | 18.2 | 18.4 | 18.4 | 18.4 | 18.4 | 18.4 | 18.4 | 18.4 | 18.4 | 18.4 | 18.4 | 18.7 | 18.9 | 18.9 | 18.9 |
| 120239 | 56153 | | | 198 | 186 | 11416 | 11416 | 11416 | 1365 | 6219 | 6219 | 110000 | 110000 | 8246 | 7380 | 7380 | 430 | 281 | 200 | 197 | 188 | 117829 | 7312 | 7312 | 7312 |
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| ABD33244 | AAS46793 | ADE84197 | ABZ10205 | AAL50548 | ABZ80711 | AAS61064 | ABL70136 | ABL32119 | ACA45063 | AAS63324 | ABL32866 | AAX20248_07 | AAX20248_06 | ABL32203 | ABK28196 | AAS45361 | AAZ35832 | AAL50551 | AAL50544 | AAL50556 | ABZ80707 | ADQ97319 | AAS61350 | ABL70402 | ABL33815 |
| Abd33244 Murine ca | Aas46793 Tumour su | Ade84197 Human lym | Abz10205 Haematopo | Aal50548 Triatoma | Abz80711 Triatoma | | Abl70136 Chemicall | | Aca45063 Prokaryot | Aas63324 Chemicall | Abl32866 Human imm | Continuation (8 of | 7 | Abl32203 Human imm | | | | | Aal50544 Plautia s | Aal50556 CrPV-like | | Adq97319 Human can | Aas61350 Human gen | Ab170402 Chemicall | Abi33815 Human imm |

ALIGNMENTS

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RRESULT 1
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Cric
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WO20
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                                                                                                                                                                                                                                                                                                                            WO2003033719-A1.
                                                                                                                                                                                                                                                                                                                                                     Cricket paralysis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                              Cricket paralysis virus derived pseudoknot
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ80710 standard; RNA; 188 BP
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IGR-IRES;
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RESULT 2
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ID AALSOS47
AC AALS
AC AALS
AC AALS
AC CrPV
KW GrPV
KW WPI
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Best Local S
Matches 188
                             The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene
                                                                                                                                                                                                                                                                                  Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CrPV-like virus; 88; higher-order structure; drug development; drug production; translational activity-promoting function; protein synthesis; structural analysis
                                                                                                                                                                                                            Claim 1; Fig 1-2; 38pp;
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Pred. No. 1.2e-46;
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                                        The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Drosophila C virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                              Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translactivity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                        Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakashima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibuya N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence
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Pred. No. 1.2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                            The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Drosophila C virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CrPV-like virus; ss; higher-order structure; drug development;
drug production; translational activity-promoting function;
                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakashima N,
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                                                                               35 G; 0 T; 72 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3e-
Score 123.6; DB 6; Pred. No. 3.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3e-27;
Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCI.
                         Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Loc Matches

Local

al Similarity 122; Conserv

Conservative

33.7%;

Score 63.4; DB 8; Pred. No. 4.2e-09; 0; Mismatches 61;

Length 190; Indels

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Gaps

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Query Match

190

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RESULT 5
ABZ80712 5
ABZ80712 1D
ABZ80 XX ABZ80 XX ABZ80 XX Pseu
DT 15-O
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CX XX (NAJ
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                                                                                The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence is black queen-cell virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translativity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudoknot; secondary structure; cell-free albumen; impurity; higher-order structure; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 34; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-2002; 2002WO-JP010447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black queen-cell virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black queen-cell virus derived pseudoknot sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI, 2003-403230/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2001; 2001JP-00319923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAAG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAT INST AGROBIOLOGICAL SCI WAKENYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; RNA; 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UAACCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UCUUAAUAAUUAGGUUAACUAUUUUAGUUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAU
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   58
                                                                proteins
A; 36 C;
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   56 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein synthesis; wheatgerm;
intergenic region; IGR-IRES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
      Other;
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                                                                                        Query Match
Best Local Simi
Matches 122;
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                                                                                                                                                                                                                                                             The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Black queencell virus RNA sequence of the invention. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001JP-00016746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2001; 2001WO-JP000641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2003
19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAAG-) NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Black queen cell virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black queen-cell virus RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL50549;
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                                                                                                                             Similarity
CAAAAAUGUGAUCUUGCUUGUAAAUAC-AAUUUUUGAGAGGUUAAUAAAUUACAAGUAGUG
                                                                                                                                                                                                            202 BP; 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 1-2; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUCAGAUUAGGUAGUCGAAAAACCUAAG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAUUU 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAUU 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAAAUGUGAUCUUGCUUGUAAAUAC-AAUUUUGAGAGGUUAAUAAAUUACAAGUAGUG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCC 121
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                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INST AGROBIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kanamori
                                                                                                                                                                                                            A; 38 C; 42 G; 0 T; 59 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                      33.7%;
65.9%;
                                                                                           0,
                                                                                        Score 63.4; DB 6;
Pred. No. 4.3e-09;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCI.
                                                                                           61;
                                                                                                                                               Length
                                                                                           Indels
                                                                                     2;
                                                                                     Gaps
                                 59
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RESULT 7
                                                                  Matches
                                                                                                 Query Match
                                                                                                                                                                          The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the himetobi P virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                                                           Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                              Sequence 187 BP; 53 A; 32 C; 39 G; 0 T; 63 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudoknot; secondary structure; cell-free protein synthesis; albumen; impurity; higher-order structure; intergenic region; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001; 2001JP-00319923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Himetobi P virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002; 2002WO-JP010447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himetobi P virus derived pseudoknot sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ80708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ80708 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NAAG-) NAT INST AGROBIOLOGICAL SCI. (WAKE-) WAKENYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2003
                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-403230/38
                                                                  100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
 15
                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 ССАСААИАИССАССААССССССССССССССССССНОПОПОСАСАПИАСОИАС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                   Similarity
                          UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUUGUAUUUA
UGAUUAGAAGUAAGAAAAUUCCUAGUUAUAUAUUUUUUAAUACUGCUACAUUUUUAAGAC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAUUU 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUAUUUUUGUAUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAG-UGGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAUU 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUG
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                  32; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA;
                                                                              24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa
                                                              0;
                                                              Score 46.4; DB 8;
Pred. No. 0.00056;
0; Mismatches 71;
                                                                                             Length 187;
                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wheatgerm;
IGR-IRES;
                                                              Gaps
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                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                      The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Himetobi P virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                            Sequence 199 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2001; 2001WO-JP000641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Himetobi P virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein synthesis; structural analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Himetobi P virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL50545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL50545 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              in druge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2001; 2001JP-00016746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAAG-) NAT
                                                                                                                                                                                 100;
                                                                                                                        15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A - CCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAUUUCAC
A-CCUAGGUGCAGCCUUGUAGUUUUUAGUGGACUUUUAGGCUAAAGAAUUUUCAC
                            GCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC 186
                                                                                         GGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAA 134
                                                                                                                      UGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCUACAUUUUUAAGAC 74
                                                                                                                                                   UGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAAUUUAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCUUAGUUAUUUAGCUUUACCGCCCAGGAUGGGGUGCAGCGUUCCUGCAAUAUCCAGGGC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCCAGGAA 134
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INST AGROBIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kanamori
                                                                                                                                                                                                                                            60 A; 33 C; 40 G; 0 T; 66 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA;
                                                                                                                                                                                              24.7%;
                                                                                                                                                                                 0,
                                                                                                                                                                                           Score 46.4; DB 6;
Pred. No. 0.00057;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                 71;
                                                                                                                                                                                                            Length 199;
                                                                                                                                                                                 Indels
                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
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                                                                                                                                                                                 Gaps
                                                           134
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RESULT 9
ABK83573/c
ID ABK83573/c
XX ABK835
XX Human;
KW Human;
KW Frequia
KW Crohn;
KW Crohn;
KW Grohn;
XX Homo s
XX W Granull
XX Homo s
XX Frequia
XX GENE-
YA (GENE-
YA (GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel diseas Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 144; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2001; 2001WO-US030821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA differentially expressed in granulocytic cells #144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2000; 2000US-0237189P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal infection; sterile inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK83573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-435328/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 88; granulocytic cell; DNA chip; bacterial infection; infection; parasitic infection; protozoal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease; psoriasis;
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CC DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where CC differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the CC expression of at least one gene in Gs; (2) screening (M3) for an agent tissue, an altergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression CC pathogen or sterile inflammatory disease using the gene expression CC pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of subject to a pathogen or sterile inflammatory disease, by detecting the level of cf expression of the gene is indicative of inflammation; (4) treating CC response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile (CC response in a subject, exposure of a subject to a pathogen or sterile (CC response in a subject, exposure of a subject to a pathogen or sterile (CC response in a subject, exposure of a subject to a pathogen or sterile (CC response in a tissue, an allergic response in a tissue, an allergic response in a subject to a pathogen or sterile (CC response) in a tissue, an allergic response in a subject (e.g. cexposure of a subject to a pathogen or sterile inflammation (a) treation (cc exposure of a subject to a pathogen or sterile inflammation (a) treation (cc exposure of a subject of modulating GCA preferably in an (cc inflammation in a tissue, an allergic response in a subject, (cc exposure of a subject to a pathogen or sterile inflammation (e.g. cc psocially chronic) in a tissue, an allergic response in a subject, (cc exposure of a subject to a pathogen or sterile inflammation (e.g. cc psocially chronic) in a tissue, an allergic response in a subject, (cc exposure of a subject to a pathogen or sterile infla The invention relates to detecting (M1) granulocyte (GC) (GCA), by detecting the level of expression of gene(s) (infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above (Gs) identified activation λÂ

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RESULT 10
ACH45871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
     The invention relates to an isolated polynucleotide comprising any one of 30043 cDNA sequences, appearing as Aciti2789-Aciti50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding the reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide
                                                                                                                                                                         New polynucleotide sequences obtained as hybridization probes, as oligomers mapping, in the recombinant production
                                                                                                                                       Claim 1;
                                                                                                                                                                                                                              WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                        Drmanac
                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003073623-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                          (LABA/)
(STAC/)
                                                                                                                                                                                                                                                                                                                                                            30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                                                                               17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human foetal brain cDNA #6596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 130263 BP;
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                                                                                                                                                                                                                                                                                STACHE-CRAIN
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; sequencing by hybridisation; SBH; expressed sequence mapping; biodiversity; genetic disorder.
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77
                                                                                                                                                                                                                                                                                                                        LABAT I.
                                                                                                                                                                                                                                                                                                                                   DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                     SEQ ID NO 33083; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTTGTGAAAACAATTTGTTGTTTTACCTAACAAATGTA 97936
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llarity 30.6%;
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Pred. No. 0.38;
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                                                                        26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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30-JUN-2000;
07-JUL-2000;
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07-JUN-
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                                                                                                                                                                                                     11-JUL-2000;
14-JUL-2000;
                                                                                                                                                                                                                                                      07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000;
17-MAR-2000;
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-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
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2000US-0209467P.
2000US-0214886P.
2000US-0216880P.
2000US-0216880P.
2000US-0217487P.
2000US-0217487P.
2000US-0217496P.
2000US-0217496P.
2000US-0217496P.
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2000US-02217496P.
2000US-02252114P.
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2000US-0190076P.
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2000US-0186350P.
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Pred. No. 0
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ine; metastasis; ds.
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14-AUG-14-AUG-14-AUG-

2000US-0225268P

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CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cotivity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention, diagnossis and creatisms and polynucleotides may be used in the prevention. Grant treatment of diseases associated with inappropriate (I) expression. For considering the production of compression by rectifying mutations or deletions in a patient's genome concentrated the activity of (I) by expressing inactive proteins or to concentrate affect the patients own production of (I). Additionally, (I) concentrated with expressing the concentrate acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, concers and cancer metastases of haematopoietic decides, especially concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 corpresent sequences used in the exemplification of the present invention.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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08-DEC-2000
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17-NOV-2000;
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08-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                               Sequence 43938
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 32028; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                                                             c acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and metastasis
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2000US-0249215P.
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2000US-0249265P.
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2000US-02492997P.
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2000US-0249210P.
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2000US-0246609P.
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                                                 BP; 12772 A; 9656 C; 9206 G; 12304 T; 0 U; 0 Other;
 20.5%;
33.5%;
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 Score 38.6; DB 4; Pred. No. 0.7;
                  Length 43938;
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14-AUG-2000
14-AUG-2000
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14-AUG-2000
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01-SEP-2000
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06-SEP-2000
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03-NOV-2000
03-NOV-2000
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08-NOV

2000US-022547PP
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2000US-022575PP
2000US-022575PP
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2000US-0227009P
2000US-022709PP
2000US-0229343P
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2000US-023943P
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2000US-023124997P
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2000US-0246523P
2000US-0246523P

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RESULT 12
AAK77217
IDD AAK777217
XX AAK77
XX AAK77
XX O7-N
DT 07-N
DE Huma
XX Huma
XX Huma
XX Huma
XX Hom
XX PN WO2
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04-FBB-2000
24-FBB-2000
02-MAR-2000
16-MAR-2000
11-MAR-2000
11-MAR-2000
20-JUN-2000
20-JUN-2000
20-JUL-2000
21-JUL-2000
22-JUL-2000
23-JUL-2000
23-JUL-2000
23-JUL-2000
30-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK77217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157182-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUUAAGAAA 181
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2000US-0186354P.
2000US-0186354P.
2000US-0198123P.
2000US-0205515P.
2000US-02148867P.
2000US-02148867P.
2000US-02148867P.
2000US-02148867P.
2000US-02117487P.
2000US-02117487P.
2000US-0218290P.
2000US-02284518P.
2000US-0228519P.
2000US-0225261P.
2000US-0225261P.
2000US-0225261P.
2000US-0225261P.
2000US-0225261P.
2000US-02252688P.
2000US-0226688P.
2000US-0226688P.
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2000US-022668P.
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2000US-022688P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:32029
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    14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
29-SEP-2000
20-OCT-2000
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02-OCT-2000
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03-OCT-2000
03-OCT-2000
03-OCT-2000
03-OCT-2000
03-OCT-2000
03-NOV-2000
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01-SEP-2000
01-SEP-2000
05-SEP-2000
06-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
14-SEP-2000;
  2000US-023404P

2000US-023401P

2000US-0233063P

2000US-023423P

2000US-023423P

2000US-023499PP

2000US-023498PP

2000US-0235834P

2000US-0235834P

2000US-023636P

2000US-023703P

2000US-0240960P

2000US-0241785P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024677P

2000US-024652P

2000US-024652P

2000US-024652P

2000US-024651P

2000US-0246611P

2000US-0246920PP

2000US-0246920PP

2000US-0246920PP

2000US-0249200PP

2000US-024920PP

2000US-024920PP

2000US-0249211P
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2000US-0229349

2000US-0229349

2000US-02304379

2000US-02312439

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2000US-0231249

2000US-0231249

2000US-02320809

2000US-02320809

2000US-02323999

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2000US-02323999

2000US-02323999

2000US-02324019

2000US-02334019

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                                                                                                                                                                                                                                                                                                                                  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) camino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) correctins and polynuclectides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased correction by rectifying mutations or deletions in a patient's genome contract affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) colynuclectides may be used to produce the secreted (I), by inserting the colynuclectian into a host cell and culturing the cell to express the correctin. (I) proteins and polynuclectides may be used to prevent, cancers and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                         Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000; 2000US-024929P-
17-NOV-2000; 2000US-024929P-
17-NOV-2000; 2000US-0250160P-
01-DEC-2000; 2000US-0250160P-
01-DEC-2000; 2000US-025198BP-
05-DEC-2000; 2000US-025198BP-
05-DEC-2000; 2000US-025198BP-
05-DEC-2000; 2000US-025198BP-
06-DEC-2000; 2000US-0251856P-
08-DEC-2000; 2000US-0251868P-
08-DEC-2000; 2000US-0251868P-
08-DEC-2000; 2000US-0251869P-
08-DEC-2000; 2000US-0251989P-
08-DEC-2000; 2000US-025198P-
08-DEC-2000; 2000US-025198P-
08-DEC-2000; 2000US-025198P-
08-DEC-2000; 2000US-025198P-
08-DEC-2000; 2000US-025499P-
08-DEC-2000; 2000US-025499P-
08-DEC-2000; 2000US-025499P-
08-DEC-2000; 2000US-025499P-
08-DEC-2000; 2000US-025499P-
08-DEC-2000; 2000US-025499P-
                                                                                                                                                                                                                                                                                                     Sequence 45017 BP; 12919 A; 10037 C; 9566 G; 12495 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 32029; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000;
                                                                                                                                                    8574
                                                                         8634
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                                   129
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                                                                                                                                                                                                                             58;
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                                                                                                                                                                                        9 UGAUCUUGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                 Similarity
AAATTAAGTCACATTTTTAACTTTTTTTGTGTGAATTTTTTCTACAGTTCTCAAAATTTT
                                                                                                            UAUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUC 128
                                                                                                                                                    TCATCTCGGGTCTTAAAATAAAATTCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA
                                 Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0249218P.
2000US-0249244P.
2000US-0249245P.
2000US-0249264P.
2000US-0249265P.
2000US-0249299P.
2000US-0249309P.
2000US-0249300P.
2000US-0249300P.
                                                                                                                                                                                                                             Conservative
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2000US-0249215P.
2000US-0249216P.
2000US-0249217P.
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                                                                                                                                                                                                                                             20.5%;
33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben
                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                           Score 38.6; DB 4; Length 45017; Pred. No. 0.71;
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                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                             74;
                                                                                                                                                                                                                             Indels
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                                                                                                                                                    8633
                                                                           8693
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RESULT 13
ADQ97028
ID ADQ97
XX ADQ97
XX ADQ97
XX ADQ97
XX CytoE
XX CytoE
XX CytoE
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
XX YO200
XX Homo
XX Clair
XX Homo
XX Clair
XX Clair
XX The I
CC The I
CC ADQ91
CC data
CC data
CC data
CC data
CC data
CC Gtp.1
RESULT 14
AAL60324
ID AAL60
XX
AC AAL60
XX
AC AAL60
XX
DT 27-AU
DX
XX
Aphid
XX
ALPV;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or trocancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 84476 BP; 22346 A; 17371 C; 17200 G; 27559 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.
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                               Aphid lethal paralysis virus (ALPV)
                                                                 27-AUG-2003
                                                                                                  AAL60324;
                                                                                                                                   AAL60324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2002; 2002US-00330773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2003; 2003WO-US041389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAGR-) SAGRES DISCOVERY INC
                                                                                                                                                                                                                                                                                83462 AAATTÄAGTCÄCATTTTTÄACTTTTTTGTGTGAÄTTTTTTCTACAGTTCTCAAAATTTT
                                                                                                                                                                                                                                                                                                                                                   83402 TCATCTCGGGTCTTAAAATAAAATTCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA 83461
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                                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                   standard;
                                                                                                                                                                                                                                                 CAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                ugaucuugcuuguaaauacaauuuuugagagguuaauaaaauuacaaguagugcuauuuuuu 68
                                                                                                                                                                                                                  UAUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGGCCCCACAAUAUC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malandro
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 20.5%; Score 38.6; DB 33.5%; Pred. No. 0.87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MS;
                                                                                                                                   9829
                                                                                                                                                                                                                                                                                                                                                                                                                   38;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                  RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IJ
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 84476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and/or treating
                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                  83571
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밁 S 멂 S 멹 8

ALPV; Aphid lethal paralysis virus; homopterous insect; floriculture;

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RESULT 15
ABK31350
ID ABK313
XX ABK31
XX ABX31
X
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Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel RNA derived from an ALPV (Aphid lethal paralysis virus). ALPV RNA is useful for controlling homopterous insects such as aphids or white flies. It is useful in the research concerning aphids and for controlling aphids and for controlling aphids and for detecting aphids and for preparing a monoclonal antibody against antigen which is synthesised for preparing a monoclonal antibody against antigen which is synthesised in virto. The invention is also useful in gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid derived from aphid lethal paralysis virus, useful detecting ALPV-viruses, for preparing a monoclonal antibody against antigen, in research concerning aphids and for controlling aphids.
                                                                                                                                                                                                                                                    Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cance antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK31350
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Search completed: December 22, Job time : 273.684 secs

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CC The present invention relates to chemically modified DNA sequences of cc signal transduction associated genes. The DNA sequences are chemically cc modified using a solution of bisulphite, hydrogen sulphite or disulphite. CA Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method cc for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be cc obtained from cells or cellular components which contain DNA, e.g. cell clines, bioppies, blood, sputum, stool, urine, cerebral-spinal fluid, cc tissue embedded in paraffin such as tissue from eyes, intestine, kidney, can be can all their possible combinations. The sequences of the invention are cuseful for the diagnosis and therapy of diseases associated with signal cr transduction e.g. solid tumours and cancer. ABK31154 represent chemically pretreated genomic DNA sequences of the printed security sequence date for this patent did not form part of the printed cc sequence date for this patent did not form part of the printed sequence con the contain but was obtained in electronic format directly from the contains a patent office.
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01-SEP-2000; 2000DE-01043826.
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    TAAATTGTGGTAAAAGTTATATATGGTGGTTTATATTTG 1990
                                                                                                                                                              TITITITTTGATATATATTTGTCGTTGTATATAACGTGATGTATTTCGTT 1951
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| | | BB818094 BB818094 |

ALIGNMENTS

TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CO153155 LOCUS DEFINITION ORIGIN REFERENCE FEATURES Query Match Best Local Similarity Matches 95; Conserv AUTHORS source Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophildae; Drosophila. 1 (bases 1 to 433) CO153155 433 bp mRNA linear EST 05 EN01401.5prime Exelixis FlyTag MNO8 BlueScript Drosophila melanogaster cDNA clone EN01401 5, mRNA sequence. CO153155 CO153155.1 GI:48907156 Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Pax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu plate: EN.14 row: A column: 1 High quality sequence stop: 383. Location/Qualifiers Exelixis FlyTag EST Project MN08 Library Unpublished (2004) Nakanishi,M., Muzong,C., Peterson,E., Laufer,A., Leung,W., Platt,D. and Swimmer,C.Contact: Stapleton, M. Drosophila melanogaster (fruit fly) 66.6%; Score 125.2; DB 7; llarity 51.1%; Pred. No. 1.5e-24; Conservative 53; Mismatches 38; /cell line="mbn2" /clone lib="Exelixis FlyTag MNO8 BlueScript" /clone Vector: pBluescript; Site 1: NotI; Site 2: oligodT primed from LPS induced mbn2 cell line." /organism="Drosophila melanogaster" /mol_type="mRNA" /db xref="caxon:7227" /clone="EN01401" Insecta; Pterygota; era; Muscomorpha; Length 433; 0; EST 05-OCT-2004 Gaps

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JOURNAL
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CO153454
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Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                         128 TTTTAATAATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCTATTGGCAGCCCCAT 187
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
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Plate: EN.20 row: A column: 10
High quality sequence stop: 412.
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Nakanishi, M., Muzong, C.,
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CO153454.1 GI:48907455
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                                                                                                                                  UUACCU 188
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                                                                           253
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/clone_lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site 1: NotI; Site_
/note="Vector: pBluescript; Site 1: NotI; Site_
oligodT primed from LPS induced mbn2 cell line.
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|mol type="mRNA"
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|clone="EN02010"
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51.1%;
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Pred. No. 1.6e-24;
3; Mismatches 38;
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 539)
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CO337794 CO337794.1 GI:49398069
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Email: http://www.fruitfly.org/EST,
Plate: EN.27 row: E column: 8
High quality sequence stop: 401.
Location/Qualifiers
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 490)
Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Pland Swimmer, C.
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One Cyclotron Rd, Berkeley, CA 94720, USA
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/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EN02756"
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Pred. No. 1.6e-24;
3; Mismatches 38;
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EST.
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Apium graveolens
Apium graveolens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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351 bp mRNA linear EST 10-SEP-:
BIP0018 BIP up-regulated phloem library after plant infestation
with Myzus persicae Apium graveolens cDNA, mRNA sequence.
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                                                                                                                                                            Systemic response to aphid infestation by Myzus phloem of Apium graveloens Plant Mol. Biol. 57 (4), 517-540 (2005)
                                                                                                                                                                                                                                                asterids; campanulids; Apiales; Apiaceae; Apioideae; superclade; Apium clade; Apium.

1 (bases 1 to 351)

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1 (boses 1 to 351)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exelixis FlyTag EST Project MN08 Library Unpublished (2004) Contact: Stapleton, M.
                                                                Route de St-Cyr 78026
                                                                                                     Laboratoire de Biologie Cellulaire
                                                                                                                             Contact: Dinant
                                                                                                                                                                                                                                   Kusiak, C. and Dinant, S
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                      33130833047
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  Sylvie.Dinant@versailles.inra.fr.
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/note="Vector: pBluescript; Site 1: NotI; Site 2:
oligodT primed from LPS induced mbn2 cell line."
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/mol_type="mRNA"
/db xrefs"taxon.7227"
/clone="EN15317"
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51.1%; Pred. No. 1.6e-24;
tive 53; Mismatches 38; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
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BIP0433 BIP up-regulated phloem library after plant infesurth Myzus persicae Apium graveolens cDNA, mRNA sequence.
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Apium graveolens
                                                                                                                                                                 Email: Sylvie.Dinant@versailles.inra.fr
Location/Qualifiers
                                                                                                                                                                                                                                                       Route de St-Cyr 78026 Versailles Cx
                                                                                                                                                                                                                                                                                                                     Contact: Dinant
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1 (bases 1 to 351)
                                                                                                                                                                                                               Tel: 33130833047
Fax: 33130833099
                                                                                                                                                                                                                                                                                                 Laboratoire de Biologie Cellulaire
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/clone_lib="BIP up-regulated phloem library after plant
/clone_lib="BIP up-regulated phloem library (SCH)
/note="Vector: pCMIZINE persicae"
/note="Vector: pCMIZINE por Substractive library (SCH)
enriched in cDNA coming from Apium graveolens phloem
tissue and up-regulated by Myzus persicae infestation.
This sequence has been generated in the framework of the
French plant genomics program Genoplante
(http://www.genoplante.org and
http://genoplante-info.infobiogen.fr)."
/tissue_type="phloem"
/dev_stage="adult plant"
/clone_lib="BIP up-regulated phloem library after plant
                                                                                   /mol_type="mRNA"
/cultivar="Vert d'Elne"
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/mol_type="mRNA"
/cultivar="Vert d'Elne"
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/tissue_type="phloem"
                                                                db_xref="taxon:4045
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near EST 10-SEP-2004 plant infestation

Myzua

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm.
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bohlmann@msl.ubc.ca
Plate: WS01026 row: D co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Picea sitchensis
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/db_xref="taxon:3332"
/clone="WS01026 D16"
/sex="Hermaphrodite"
/fissue_type="Young root growth (terminal 1-3 cm) and old root growth (distal to terminal 1-3 cm) tissues"
/dev_stage="three year old clonal trees grown under greenhouse conditions in standard potting soil mixture."
/lab_host="E. coli DH10B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infestation with Myzus persicae"
/note="Vector: pCRI-TOPO; Substractive library (SSH)
enriched in cDNA coming from Apium graveolens phloem
tissue and up-regulated by Myzus persicae infestation.
This sequence has been generated in the framework of the
French plant genomics program Genoplante
(http://www.genoplante.org and
http://genoplante-info.infobiogen.fr)."
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Picea sitchensis"
/mol_type="mRNA"
/cultivar="Gb2-229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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33.7%; Pred. No. 0.042;
tive 35; Mismatches 79; Indels
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clone
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Picea.
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ORGANISM
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BX159895
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Best Local S
Matches 39
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Best Local Similarity
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                                                                      217 TCTTTÄAÄTTÄTAATGTTÄGGACTÄTÄÄÄÄAATTÄÄTTTATATGCTATTAGTÄGTÄGGCTT 158
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62 AUUUUUGUAUUUAGGUUAGCUAUUUAGGUUUACGUUCCAGGAUGCCUAGUG 112 :::| :::| |::| ::| |::| ::| || ||:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAG 131

    UGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUAGGUU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of BAC 125P2. 125P2 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13-MAR-2003) The Sanger Institute, V
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humphray, S.J., Huckle, E. and Durham, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1. (bases 1 to 755)
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Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio genomic clone DKBY-125P2, genomic survey sequence.
BX159895
                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                       /clone="DKEY-125P2"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
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                                                                                                                                                                                            21.6%;
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38.9%; Pred. No. 0.86;
                                                                                                                                                                        28;
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Pred. No. 1.2;
28; Mismatches
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                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Watahiki,M., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira, and Dayasaki,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Numasaki, R., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB746609 RIKEN full-length enriched, adu cDNA Clone F530101N20 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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/clone lib="RIKEN full-length enriched, adult male kidney" /clone lib="RIKEN full-length enriched, adult male kidney" /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research foroup in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                             tissue_type="kidney"
'dev_stage="adult"
'lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="F530101N20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                 gex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                      type="mRNA"
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Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudico
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                      DNA is from a doubled haploid provided 
Seq primer: TF 
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                             Other_GSSs: BOMAB63TR
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                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
                   Similarity
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length
                                                                                                                                                                                                                        Location/Qualifiers
1. .588
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/note="Vector: pHOS1; Site_1: B
genomic DNA inserted into pHOS1
                                                                                                                                                                     /mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                      organism="Brassica oleracea"
                                                                                                                                                      db_xref="taxon:3712"
                                                                                                                                     clone="BOMAB63"
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Pred. No. 7.1;
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CC963421/c
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     Burvey sequence.
BH517849
BH517849.1 GI:17725939
GSS.
                                                                          BH517849 777 bp
BOGUU79TF BOGU Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtcwn@tigr.org
DNA is from a doubled haploid
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other_GSSs: BOICV54TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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GSS.
Brassica oleracea
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="BOICV54"
/clone lib="BOICV54"
/clone lib="DIA 1.6 KB nuc"
/note="Vector: pH052; Site 1: I
/notea="Vector: pH052; Site 1: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="TO1000DH3"
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_nuc Brassica
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pHOS2 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                 Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EN.158 row: F column: 2
                                                                                                                            Contact:
                                                                                                                                                                                                                 Neoptera; Endopterygota; Diptera; Brach
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 453)
                                                                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda;
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melanogaster cI
                                                                                                                                                Unpublished (2004)
                                                                                                                                                             Exelixis FlyTag EST Project MN08 Library
                                                                                                                                                                                    and Swimmer, C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 777)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: BOGUU79TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea
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                                                                                                                            Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BOGUU79"
/clone lib="BOGU"
/clone lib="Soctor: pHOS1; Site 1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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1. .777
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                                                                                                                                                                                                                                                                                                                                                  GI:49398359
sequence
                                                                                                                                                                                                                                                                                                                                                                                      cDNA clone
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stop:
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FlyTag MN08 BlueScript Drosophila
EN15862 5, mRNA sequence.
                                                                                                                                                                                                Peterson, E., Laufer, A.,
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                                                                                                                                                                                                                                                     Brachycera;
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                                                                                                                                                                                                                                                                       Pterygota;
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TITLE
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CZ696233/c
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Query Match 19.7%;
Best Local Similarity 36.6%;
Matches 37; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AUUUACCU 188
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OC_Ba000
5', genor
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                                                                                                                                                                                                                                                                                    FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0009 row: L column: 24
Seq primer: TAA TAC GAC TCA CTA TAG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5', genomic survey sequence.
CZ696233
CZ696233.1 GI:71095381
                                                                                                                                                                                                                                                                                                                                                                                                             Arizona Genomica Inštitute
University of Arizona
Forbes Building Room 303, Tucson, AZ
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 452)
1 (bases 1 to 452)
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D., Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D., Kim, H., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza coarctata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza coarctata (Porteresia coarctata)
                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                               PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Exelixis FlyTag MN08 BlueScript" /note="Vector: pBluescript; Site 1: NotI; Site oligodT primed from LPS induced mbn2 cell line.
                                                                                   /mol type="genomic DNA"
/db xref="taxon:77588"
/clone="OC_Ba009L24"
/tlssue_type="leaves"
/dev stsge="mature"
/lab_host="DH108"
/lab_host="DH108"
/lone_lib="OC_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                  organism="Oryza coarctata"
                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:7227"
/clone="EN15862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Drosophila melanogaster"
/mol_type="mRNA"
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 ; Score 37; DB
; Pred. No. 12;
24; Mismatches
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Pred. No. 7.8;
15; Mismatches
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                                   10; Length 452;
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Zantedeschia aethiopica
Zantedeschia aethiopica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Aroideae;
Zantedeschieae; Zantedeschia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and cDNA arrays
Unpublished (2005)
Contact: Piques MC
Institut fuer Biologie II
Albert-Ludwigs-Universitaet Freiburg
Schaenzlestr. 1, D-79104 Freiburg, GERMANY.
                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 485)
Piques, M.C., Werber, M., Lino-Neto, T., Barbeta, C., Tavares, R.M.
Weisshaar, B., Pais, M.S. and Palme, K.
Gene expression analysis during Zantedeschia aethiopica floral
spathe senescence and senescence-inhibition using EST sequencia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ702451
AJ702451 ZAAE floral spathe MPIZ-ADIS-062 cDNA Zantedeschia aethiopica cDNA clone J-18-4, mRNA sequence.
                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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AJ702451
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                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                           /tissue_type="floral spathe"
/dev stage="floral spathe whitening and regreening"
/lab_host="Bscherichia coli strain TOP10"
/clone lib="ZAAE floral spathe MPIZ-ADIS-062 cDNA"
/note="Vector: pspORT1; cDNA synthesis was performed using SuperScript system (Invitrogen) and directionally-cloned (Sal I at the 5'-end and Not I at the 3'-end) into pspORT1 (U12390.1) country: Portugal:Braga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:69721"
/clone="J-18-4"
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                 22,
                 2005, 15:21:02
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Result
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Maximum Match 100%
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Perfect score:
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       22221111111111112
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1: /cgn2_6/ptodatta/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodatta/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodatta/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodatta/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodatta/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodatta/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodatta/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodatta/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodatta/1/ina/RE_COMB.seq:*
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18.2 601
18.2 173992
17.7 108169
17.3 25769
17.3 67876
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US-09-270-767-16354
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US-09-949-016-123899
US-09-949-016-12899
US-09-949-016-17154
US-09-949-016-17154
US-09-949-016-17232
US-09-949-016-17232
US-09-949-016-17232
US-09-949-016-18339
US-09-949-016-183399
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Sequence 1072, Ap
Sequence 1354, A
Sequence 17344, A
Sequence 13379, A
Sequence 12898, A
Sequence 17907, A
Sequence 17929, A
Sequence 1754, A
Sequence 172590, A
Sequence 172590, A
Sequence 1, Appli
Sequence 1309, Ap
Sequence 1299, Ap
Sequence 1299, Ap
Sequence 11902, A
Sequence 17002, A
Sequence 674, App
Sequence 674, App
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Sequence 674, App
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Sequence 17002, A
Sequence 18399, A
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Sequence 17002, A
Sequence 674, App
Sequence 18399, A
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Sequence 674, App
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Sequence 18399, A
Sequence 1836, Appl
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RESULT 2
US-09-270-767-16354
; Sequence 16354, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

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|----------|---|--|---|---|---------------------|--------------------------|--------------------|---------|--|---|------------|-------|--------|-------------------|-----------------|-----------------|---------------------|---------------------|---------------------|--|--|--|--|--|---|---|
| | | | | Query M Best Lo Matches | TYPE: DNA ORGANISM: | SOFTWARE: SEQ ID NO 1 | URREN | ILE R | NERAL PPLIC | LT 1 9-270 quenc | | 50. | 43 | 42 | 4 6 | 39 | 38 | 3 8 | 35 | u u | 32 | יי ה | 29 | 28 | 27 | 2 5 |
| 183 U | 123 AJ 640 AJ | 63 UI :: 085 | 3 AJ 520 AJ | Match Local Sin | | ARE: Pat NO 1072 | T FILIN | EFERENC | GENERAL INFORMATION: APPLICANT: Homburge TITLE OF INVENTION: | SULT 1 -09-270-767-1072 Sequence 1072, Applic | | | 30.8 | ۰, | 3 L | 3 2 | 31 | 31 | u : | . LE . C | ۲! | - :- | ٠. | 1 | -: | ٠. |
| UUACCU 1 | NUAUCCA : : NTATCCA | JUUUGUA : : TTAATA | AAUGUG : : AGATGTG | Similarity 5; Conservat | osophi 72 | PatentIn 072 145 | G DATE | E: Fil | MATION: |)72 Appli | | 16.4 | 16.4 | 4 | ທ່າ | 'n | | | | ν. Ο | 6 | | ٠.٦ | | 16.7 | |
| 188 | GGAAGC | JUUAGGU | AUCUUGO : :: ATCTTGO | y 51. Y stive | la me | Ver. 2. | : 1999- S: 6251 | e Refer | ret al Nuclei | a t | | 1332 | 1441 | 441 | 1830123 | 1830121 | 87352 | 87352 | 87352 | 52655 422592 | 601 | 601 | 10330 | 3484 | ە ھ | 0.00 |
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| | GCGGUUUUUCAGAUUAGGUAG ;; ;: : GCTTCTTATATGATTAGGTTG | UUUUUGUAUUUAGGUUAGCUAUUUAGCUUUAGGUUCCAGGAUGCCUAGUGGCAGCCCCAC | AAAAUGUGAUCUUGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAUAAAUUACAAGUAGUGCUA | Score 125.2; DB 3; Pred. No. 2.3e-30; 3; Mismatches 38; | aster | | 17 | | JENERAL INFORMATION: APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic acids and proteins of Dro | ion US/09270767 | ALIGNMENTS | 09-76 | 20 | US-08-568-310D-12 | US-10-158-865-1 | US-09-557-884-1 | US-09-949-016-15693 | US-09-949-016-12721 | US-09-949-016-12053 | US-09-949-016-13495 US-09-949-016-14182 | US-09-949-016-86428 | US-09-949-016-59923 | US-10-001-189-68 | US-09-380-090A-1 | US-09-308-090-1 | -09-949-016- |
| | SUCGAAAAACCUAAGAAAU | JGCCUAGUGGCAGCCCCAC | JAAAUUACAAGUAGUGCUA AAGAAGGAAGTAGTGCTA | Length 1345; Indels 0; Gaps | | | | , | Drosophila melanogaster | | | • | 168 | equence 12, | Sequence 1, Ap | ب بـ | 156 | Sequence 12721, | Sequence 12053, | Sequence 13495, | Sequence 86428, | Sequence 59923, | Sequence 68, Ap | Sequence 1, App | (D (| e 173 |
| | AGAAAU 182 AGAAAA 699 | CCCCAC 122 CCCCAT 639 | GUGCUA 62 : : GTGCTA 579 | Gaps 0; | | | | 1 | nogaster | | | 213, | 168 | 12, | | ٠,٠ | 156 | 15600 | 12721, A | 12053, A 12721, A | 13495, A 14182, A 12053, A 12721, A | 86428, A 13495, A 14182, A 12053, A 12721, A | 59923, A 86428, A 13495, A 14182, A 12721, A | 59922, A 59923, A 59923, A 86428, A 13495, A 114182, A 112053, A 12721, A | 1, Appli 68, Appl 59922, A 59923, A 86428, A 114182, A 114182, A 112053, A 12721, A | 111111111111111111111111111111111111111 |

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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: FRUING DATE: 2000-09-08

NUMBER: FRUING DATE: 207012

SOFTWARE: FRUING DATE: 207012
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US-09-949-016-17344
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; ORGANISM: Drosophila melanogaster
US-09-270-767-16354
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Best Local Similarity
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 16354
LENGTH: 1345
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                                                                                                                                                                     43634 AAATTAAGTCACATTTTTAACTTTTTTGTGTGAATTTTTTCTACAGTTCTCAAAATTTT 43575
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95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATATCCAGGACACCCTCTCTGCTTCTTATATGATTAGGTTGTCATTTAGAATAAGAAAA 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.5%; Score 38.6; DB 3; Length 54444; 33.5%; Pred. No. 0.079; ative 38; Mismatches 74; Indels 3;
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US-09-949-016-13379
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                                                                                                                                                                                                                                                                                                          PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/227,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-56332
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                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13379
LENGTH: 173992
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 56332
LENGTH: 601
                                                                                                                                                       Query Match
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APPLICANT: VENTER, J.
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001307
                                                                                                                                                                                                                                    TYPE: DNA
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                                    Local
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                                                                                                                 l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
  UUUUUGUAUUU 73
                                                                                                               18.2%; Score 34.2; Dilarity 32.4%; Pred. No. 3.3; Conservative 25; Mismatches
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                                                                                                                                                     Length 173992;
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; ORGANISM: Human
US-09-949-016-12898
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                                                                                           ) ORGANISM: Human
US-09-949-016-15907
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHLEMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF-
FILE REFERENCE: CL001307
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Query Match 17.7%;
Best Local Similarity 30.6%;
Matches 41; Conservative 3
                                                                                                                                                          SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15907
LENGTH: 108169
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Best Local Similarity
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                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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Score 33.2; DI pred. No. 5.7; OI Mismatches
                                           DB 3;
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  63;
                                             Length 108169;
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RESULT 9
US-09-949-016-17232/c
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; ORGANISM: Human
US-09-949-016-17154
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US-09-949-016-17154
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                    PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WITER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17154
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17232
LENGTH: 67876
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17232, Application US/09949016
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAAAAUGUGAUCUUGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCU 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 17.3%; Score 32.6; Similarity 31.6%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCAGGAGTTTTT 57801
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OF DETECTION
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; ORGANISM: Human
US-09-949-016-17232
                                                                                                                                                                                                                                  US-09-081-686-1
                                                                                                                                                                                                                                                    RESULT 11
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US-09-949-016-192590/c
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 192590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                          Sequence 1, Application US/09081686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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Patent No. 6812339
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09-949-016-192590
                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                  592 TTATAACTACATTAAAAAGAGTTTACAATATTGGAAAAAGGGCTATTGTCATAATCCACT
                                                                                                                                                                                                                                                                                                           532 TTATTATGTCTACATACATGGTAGCAAACCTATTACAAGAACAATTCTAGCCAG 479
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                                                  Wallis, Nicola G.
Shilling, Lisa K.
Wang, Min
Jaworski, Deborah D.
Ingraham, Karen A.
Yigong Ge, James
                                    Holmes, David J.
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                Zalacain,
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                Magdalena
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US-09-081-686-3
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Best Local S
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APPLICANT: Wallis
APPLICANT: Shilli
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NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
STREET: 4000 CITY: Philadelphia CITY: PA
                                                           ADDRESSEE: Dechert,
                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                           APPLICANT: Throup, John
APPLICANT: Biswas, Sanjoy
TITLE OF INVENTION: Histidine Kinase
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APPLICATION NUMBER:
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                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                         181 GGTCTAGTCATTCATATAGCTATTTATTTGACCTTTCC 218
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INVENTION:
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                                            E: Dechert, Price & Rhoads
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                                                                                                                                                                            Yigong Ge, James
Holmes, David J.
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Ingraham, Karen A.
                                                                                                                                                                                                                                          Wang, Min
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Shilling, Lisa K.
                                                                                                                                                          Zalacain, Magdalena
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28.6%; Pred. No. 1.8;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1309
LENGTH: 402
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-1309
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                             Matches
                                                                                                                                               Query Match
Best Local Similarity
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APPLICATION NUMBER: 60/048,33
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,686
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CON
OPERATING SYSTEM:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-994-2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1382 GGTCTAGTCATTCATATAGCTATTTATTTGACCTTTCC 1419
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                                                      138 AAGCTCATCAATTTCATTGTGTGCTAATATTAAGATCTCGTTAGCTATTTTCCCTAACGT 197
97 UCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGA 156
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ilarity 32.6%;
Conservative 2
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SYSTEM: Windows 95
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28.6%; Pred. No. 2.
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Pred. No. 1.3;
27; Mismatches
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; OTHER INFORMATION: n = US-09-949-016-12298
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; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-543-681A-1449/c
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                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 12298
LENGTH: 115963
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APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                       ORGANISM: Human FEATURE:
                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(115963)
                                                                                                                                                                                                                                                                                                    TYPE: DNA
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Similarity 32.6%; Pred. No. 2.1;
46; Conservative 27; Mismatches
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-10-221-613-215
US-10-310-154-25
US-10-310-154-25
US-10-311-455-1788
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177, Appl

176, Appl

177, Appl

177, Appl

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| US-10-282-122A-32933 US-10-211-455-92 US-10-211-613-20 US-10-088-750B-5 US-09-925-065A-712949 US-09-925-065A-712971 US-09-925-065A-712971 US-10-473-126-345 US-10-221-714A-519 US-10-322-281-271 US-10-312-281-271 US-10-311-455-1007 US-10-311-455-1007 US-10-325-065A-656748 US-09-925-065A-6154 US-09-925-065A-6154 US-10-311-455-1089 US-10-311-455-1089 US-10-311-455-1843 US-10-311-455-1843 US-10-311-455-1843 US-10-311-455-1843 | 7 | σ | <u>-</u> | σ | 7 | 4 | 4 | σ | 4 | ص ص | 7 | 7 | æ | .4 | 4 | 4 | 4 | 7 | 7 | 6 | 7 | |
| | US-10-221-613-386 | US-10-311-455-1843 | US-10-312-841-2 | US-10-085-959-182 | US-10-367-094-74 | US-09-925-065A-680389 | US-09-925-065A-2154 | US-10-311-455-1007 | US-09-925-065A-656748 | US-10-312-841-1 | US-10-322-281-271 | US-10-221-714A-519 | US-10-473-126-345 | US-09-925-065A-712971 | US-09-925-065A-270088 | US-09-925-065A-269502 | US-09-925-065A-712949 | US-10-088-750B-5 | US-10-221-613-20 | US-10-311-455-92 | US-10-282-122A-32933 | |
| | Sequence 386, App | Sequence 1843, Ap | Sequence 2, Appli | Sequence 182, App | 74, Appl | 680389, | Sequence 2154, Ap | Sequence 1007, Ap | Sequence 656748, | Sequence 1, Appli | 271, App | e 519, App | 345, App | 712971, | 270088, | 269502, | 712949, | 5, Appli | 20, App1 | 92, Appl | 32933, A | |

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Sequence 4. Application US/10088750B

Publication No. US20040166486A1

GENERAL INFORMATION:
APPLICANT: KANAMORI, Yasushi
ITILE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
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ITILE OF INVENTION: ACTIVITY
ITILE OF INVENTION NUMBER: US/10/088,750B
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT APPLICATION NUMBER: JP P2001-016746
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR APPLICATION NUMBER: PC7/JP01/00641
PRIOR PILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 200
TYPE: RNA
ORGANISM: Cricket Paralysis Virus
     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 САЛЛАЛИ С ОТ СТИТИТЕТ В СТАТИТЕТ В СТАТИТЕ
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                                                                                                                                                                                                                                                                                       ACAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                  UAUUUUUGUAUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAAAUGUGAUCUUGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGC 60
                                                                                                               AUUUACCU 188
                                                                                                                                                                                                                         ACAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUAAGAA
AUUUACCU 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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RESULT 2

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Sequence 6, Application US/10088750B

Publication No. US20040166486A1

GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: NAKASHIMA, Novel Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation
ITILE OF INVENTION: A NOVEL HIGHER STRUCT
ITILE OF INVENTION: A NOVEL HIGHER
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                                                                                                                Query Match
Best Local Similarity
                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER CECCETATION NUMBER (PCT/JP01/00641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/088,750B
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ORGANISM: Drosophila C Virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 ААИАИССАВВААВСССИСИСИВСЕВИЙИЙИСАВАЙИАВВИКОВАААААССИААВААН 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AAUAUCCAGGACACCCUCUCUGCUUCUUAUAUGAUUAGGUUGUCAUUUAGAAUAAGAAAA 183
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CAAAAAUGUGAUCUUGCUUGUAAAUAC-AAUUUUGAGAGGUUAAUAAAUUACAAGUAGUG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UAACCU 189
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                                                                                                            33.7%;
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                                                                       Score 63.4; DB 7;
Pred. No. 3.2e-08;
0; Mismatches 61;
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Pred. No. 1.1e-25;
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                                                                                                                                          Length 202;
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                                                                   Gaps
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CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION UNMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JF01/00641
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
INUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 199
TYPE: RNA
ORANISM: Himetobi P Virus
US-10-088-750B-2
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                                                                                                                                                                                                                                                         Sequence 778298, Application US/09925065A publication No. US20050228172A9 GENERAL INFORMATION:
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108027.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
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Best Local Similarity
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TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKASHIMA, APPLICANT: KANAMORI,
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                                                                                                                                                                                                                                                                                                                                                                                                                     135 A-CCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAAUUUCAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 всссисисиесевипиписаваннавенависвалала, спарваланина 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAUU 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46.4; DB 7;
Pred. No. 0.0027;
0; Mismatches 71;
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOPTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 33083
**EXECTH. 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
US-10-221-613-215
Sequence 215, Application US/10221613
Publication No. US20040029123A1
GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-778298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-918-995-33083
                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-918-995-33083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: Past-SEQ for Windows Version 4.0
SEQ ID NO 778298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33083, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(460)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 AÁATTÁAGTCÁCATITTTTÁACTITTTTTTGTGAÁTTTTTTTCTACAGTTCTCAAAATTTT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 UAUTUAGGUUAGCUAUTUAGCUTUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ugaucuugcuuguaaauacaauuuuugagagaguuaauaaaauuacaaguaguugcuauuuuuu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 21.1%; Score 39.6; DB 4; Length 652; Similarity 34.3%; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTCTTAATGTTTAAAAGTTAGGGTTTCCTTCCAAGATGGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uuguauuuagguuagcuauuagguuuagguuccaggaugcc 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HITTGATTATTTTTGAAAATAAAGTTAAAAAATTTAAATAAAATCCAAGTATAACCTGTT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      нисискиестистичения по выправнительной по выстраннительной по выправнительной по выстраннительной по выс
                                                                                                                                                                                                                                                                                            CAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAGGUAGUCGAAAAACCUUAAGAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATCTCGGGTCTTAAAATAAAATTCAAATGTATAGAAAACTGAAGGAGTCACATTTTAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.5%;
33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.6; DB Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBTAINED
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; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
SEQ ID NO 215
; LENGTH: 5504
; TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No. US20030233670A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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APPLICANT:
APPLICANT:
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             APPLICANT:
                                                            APPLICANT:
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DE 10013847.00
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK, ALexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OP INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REFERENCE: 5013.1004
                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/221,613
CURRENT FILING DATE: 2002-09-13
                                                                                           APPLICANT:
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APPLICANT
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2000-04-06
2000-04-07
2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1952 TÄÄATTGTGGTÄÄAAGTTATATATGGTGGTTTÄTÄTTTG 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1832 ATATATGGAATTTTATTATAAATATAATATTGTTGGATTGTATAATTGAAATTGGTGAT 1891
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 CAAUAUCCAGGAAGCCCUCUCUGCGGUUUUUUCAGAUUAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AUUUUUUGUAUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTTTTTTGTTTTGAATATATATTTGTCGTTGTATATAATATAACGTGATGTATTTCGTT 1951
                                                                                                                                                                                                                                                                                                                                               Edgerton, Michael D
                                                                                                                                                                                                                                                   Ball,
                          Kretzmer, Keith A
Laccetti, Lucille B
                                                            Jung, Vincent
                                                                                        Galligan, Meghan M
Hinchey, Brenda S
Huang, Shihshieh
                                                                                                                                     Dong, Jinzhuo
Duff, Stephen M.
                                                                                                                                                                   Deng, Molian
                                                                                                                                                                                       Boddupalli, R
Deikman, Jill
                                                                                                                                                                                                                        Bell, Erin
                                                                                                                                                                                                                                                                  Agarwal, Ameeta
Ahrens, Jeffrey
                                                                                                                                                                                                                                                                                                     Ruff,
                                                                                                                                                                                                                                                                                                                 Chomet, Paul S. Adams, Thomas H
                                                                           Johnson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
             Chao-Qiang
                                                                                                                                                                                                                                                                                                   Thomas G.
                                                                                                                                                                                                                                                     James
                                                                       G. Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.9%; Score 37.4; I
23.3%; Pred. No. 4.4,
tive 46; Mismatches
                                                                                                                                                                                                      Raghava
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Lin, Jie-Yi

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APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses The
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 25
LENGTH: 6440
                                               ; TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-10-732-923-76
                                                                                                                                                                                                                                                                                                              RESULT 9
US-10-732-923-76/c
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                                                                                                                        Sequence 76, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:
APPLICANT: EGGETCON, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERBYCE: 38-15 52796 C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR PILING DATE: 2003-12-04
NUMBER OF SEQ ID NOS: 24149
SEC ID NOS: 24149
                                                                                                               SEQ ID NO 76
Best Local Similarity
                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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LOCATION: (1552)..(6087)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                LENGTH: 6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 19.4%; Score 36.4; DB 6; Length 6440;
Similarity 31.9%; Pred. No. 9.1;
30; Conservative 28; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                              UUUGUAUUUAGGUUAGCUAUUUAGCUUUACGUUC 98
                                                                                                                                                                                                                                                                                                                                                                                  TTTTTCTATCTTTTAGCTAAGGTTCCTAACGTTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang, Qiang
Zhao, Yajuan
Zhou, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xin, Znangu
Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang, Chunzhi
Zeng, Xiaoping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, Haiyun
Xin, Zhanguo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vidya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McKiel, Christine L.
Miller, Philip W.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tennesen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parnell, Laurence D. Start, William G.
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Malloy, Kathleen A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dan
19.4%;
Score 36.4; DB Pred. No. 9.1;
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             9
            Length 6440;
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US-10-437-963-96143
Sequence 96143, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      RESULT 11
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US-10-078-770-53
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CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR APPLICATION NUMBER: 60/159,401
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-0-0-11
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-0-0-11
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LENGTH: 2480
                                               APPLICANT:
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                                                               APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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                            APPLICANT:
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APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/143,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: cDNAS Encoding Polypeptides FILE REFERENCE: BB-1365 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                        2278 TTTTTGTÁAGTÁGTGTÁGGTTGGTÁGTGATTGGGTĆĆÁGATTG 2320
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                                                                                                                                                                                                                                                                                                                                                              63 uuuuuquauuuagguuagcuauuuagcuuuacguuccaggaug 105
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Similarity 36.9%; Pred. No. 9.2;
38; Conservative 23; Mismatches
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Boukharov, Andrey A.
Barbazuk, Brad
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Sequence 1788, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                        RESULT 13
US-10-221-613-312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1788
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Sequence 312, Application US/10221613 Publication No. US20040029123A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1788
LENGTH: 7312
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LENGTH: 3898
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ORGANISM: Oryza sativa
FEATURE:
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l Similarity 36.9%;
38; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.9%; Score 35.6;
25.6%; Pred. No. 16;
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US-10-221-613-312
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DE 1001958.8
DE 1001958.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2001-03-15
2000-04-06
2000-04-07
2000-06-30
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NUMBER OF SEQ ID NOS: 428
SEQ ID NO 312
LENGTH: 7312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAWORI, Yasushi
TITLE OF INVENTION: A kovel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/JP01/00641 PRIOR FILING DATE: 2001-01-31
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
FILE REFERENCE: 5013.1004
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CURRENT FILING DATE: 2002-09-13
                                                                                                                                                                                                                                                                                                                        LENGTH: 200
TYPE: RNA
ORGANISM: Plautia Stali Intestine Virus
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                                          29
                                                                                               28 ААИՄИИGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUGUAUUUAGGUUAGCUAUUUA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ИСИИССИИСИАЛАНИАСЛАНИИИСАСЛЕСИИЛАНИАЛЬНИКА СТАТОВ ИЗВЕТИТЕТ В ИСИИССИВЕНИИ ПО В ИСИИСТВИТЕТ В ИСИ
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                                    AAAUUUCGAGGUUAAAAAUAGUUUUAAUAUUGCUAUAGUCUUAGAGGUCUUGUAUAUUUA
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25.6%; Pred. No. 16;
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                                                                                                                                                                                              Score 34.6;
Pred. No. 7
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Sequence 10, Application US/10088750B

| Publication No. US20040166486A1 |
| GENERAL INFORMATION: APPLICANT: NAKASHMA, Nobuhiko |
| APPLICANT: KANAMORI, Yasushi |
| TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation |
| TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation |
| TITLE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation |
| TITLE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation |
| TITLE OF INVENTION: A NOVEL Higher-Order Structure With Promoting Translation |
| TITLE OF INVENTION: A NOVEL HIGHER: US/10/088,750B |
| CURRENT FILING DATE: 2001-015
| PRIOR APPLICATION NUMBER: UP P2001-016746 |
| PRIOR APPLICATION NUMBER: UP P2001-016746 |
| PRIOR APPLICATION NUMBER: PCT/JP01/00641 |
| PRIOR APPLICATION UNMBER: PCT/JP01/00641 |
| PRIOR APPLICATION UNMBER: PCT/JP01/00641 |
| PRIOR FILING DATE: 2001-01-31 |
| NUMBER OF SEQ ID NOS: 12 |
| SEQ ID NO 10 |
| SEQ ID NO 10 |
| LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NA
CRGANISM: Unknown
CRGANISM: Unknown
FEATURE:
FOTHER INFORMATION: The sequence is used only to illustrate secondary structures
CHIER INFORMATION: predicted by a computer program, MFOLD, as shown in Fig. 3.
US-10-088-750B-10
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Search completed: December 22, 2005, 16:21:11 Job time : 442.609 secs
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Best Local Similarity
Matches 64; Conserv
                                                                                                                         169 UACUUACCACACÁAGÁUGGACCGGAGCAGCCCUCCAÁUÁUCUAGUGUACCCUC 221
                                                                                                                                                                                                                                                               109 AAAUUUCGAGGUUAAUAAAGUUUUAAUAUUCCUAUAGUCUUAGAGGUCUUGUAUAUUUA 168
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                                                                                                                                                                        88 GCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAGGAAGCCCUC 140
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Maximum Match 100%
Listing first 45 summaries
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               0222111111111
92109876549210987654321
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                                                                                                                                                                                                                                                                                                           Published Applications NA New:*

1: /cgn2_6/ptodata/1/pubpna/US08 NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06 NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07 NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07 NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10 NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10 NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11 NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US11 NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11 NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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Match Length DB
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17.7 1132
16.4 1332
16.4 175416
16.3 120096
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16.2 340010
16.1 173115
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188
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US-10-750-185-41319

US-10-873-528-158

US-10-873-528-213

US-11-121-086-43

US-11-121-086-24

US-11-121-086-24

US-11-122-978-3

US-11-122-978-3

US-11-129-978-3

US-11-129-978-3

US-11-194-246-129

US-11-194-246-129

US-11-194-246-129

US-10-750-185-57886

US-10-750-185-57886

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US-10-750-185-57886

US-10-750-185-57886

US-10-750-185-57886

US-10-750-185-57886

US-10-750-185-5812

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Sequence 47569, A Sequence 47569, A Sequence 138, Appl Sequence 43, Appl Sequence 55, Appl Sequence 55, Appl Sequence 47264, Appl Sequence 373, Appl Sequence 373, Appl Sequence 47264, A Sequence 57886, A Sequence 5129, App Sequence 5129, Appl Sequence 5129, Appl Sequence 5186, A Sequence 5186, A Sequence 5122, A Sequence 41669, A Sequence 416482, A Sequence 46482, A Sequence 4338, A Sequence 4374, A Sequence 53110, A Sequence 53174, A Sequence 59748, A Sequence 29748, A Sequence 59748, A Seque
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| 28. 28. 2 | 28.4 | 28.4 | 28.4 | 28.4 | 28.4 | 28.4 | • | 28.6 | | 28.6 | | | 28.8 | | | 28.8 | | 28.8 | 28.8 | 28.8 |
| 15.0 15.0 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.2 | 15.2 | 15.2 | 15.2 | 15.2 | 15.2 | 15.3 | 15.3 | 15.3 | 15.3 | 15.3 | 15.3 | 15.3 | 15.3 |
| 1143 1300 | 207908 | 7785 | 3407 | 2737 | 1819 | 1766 | 387780 | 13179 | 5316 | 2028 | 1667 | 948 | 193084 | 28277 | 5068 | 4996 | 3659 | 3608 | 3583 | 3536 |
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| Sequence Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| 59641, 46866, | 21, Appl | 65, Appl | 48968, A | 63285, A | 29496, 1 | 29085, A | 13259, 1 | 13394, A | 38891, 1 | 59633, A | 25855, A | 55839, A | 82, Appl | 13241, A | 164, App | • | 127, App | 129, App | 124, Apr | idy 'czr |

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RESULT 1

US-10-750-185-41319

Sequence 41319, Application US/10750185

Sequence 41319, Application US/10750185

Publication No. US20050266603A1

GENERAL INFORMATION:

APPLICANT: MATIGNOWICS, INC.

APPLICANT: MATIS, Stephen

APPLICANT: MATIS, STEPHEN
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US-10-873-528-168

Sequence 168, Application US/10873528

Publication No. US20050276814A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics Limited APPLICANT: Gilbert, Christophe FG APPLICANT: Hansbro, Philip M TITLE OF INVENTION: Proteins FILE REFERENCE: PMC/P21129WO

CURRENT APPLICATION NUMBER: US/10/873,528

CURRENT FILING DATE: 2004-06-23

PRIOR APPLICATION NUMBER: US/09/769,787

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: GB 9816337.1

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 388

SOFTWARE: Patentin Ver. 2.1

TYPE: DNA
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TYPE: DNA
ORGANIZM: Bovine 19866881500383
-10-750-185-47569
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION OF SEQ ID NOS: 64922
SOPTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae 10-873-528-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                  16.4%; Score 30.8; DB 6; Length 1332; Local Similarity 28.6%; Pred. No. 3.7; ndels 0 28; Conservative 28; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 17.7%; Score 33.2; DB 6; Local Similarity 27.5%; Pred. No. 0.62; les 28; Conservative 31; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1042 TATATTTAGGTGAGAATCATAGTTTTACCTTTAAAAAAGCCT 100:
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                                                                                   67 GGTCTAGTCATTCATATAGCTATTTATTTGACCTTTCC 104
                                                                                                                            62 AUUUUUGUAUUUAGGUUAGCUAUUUAGCUUUACGUUCC 99
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                                                                                                                                                                       7 AAAAATCCTAAATTATTAACCAAGTCTTTTTAAGAAGTTTTGCAATTCTAGGTGGTGTT 66
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BATES, Stephen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
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                                                                                                                                                                                                                                            SEQ ID NO 43
ELENGTH: 175416
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-43
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CURRENT FILING DATE: 2004-06-23
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
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SEQ ID NO 213
LENGTH: 1332
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Matches
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Best Local :
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APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Streptococcus pneumoniae
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Local Similarity 27.8%; Pred. No. 28;
1es 25; Conservative 28; Mismatches
60719 TITATTTATTTAATTTATTCATTTAT 60690
                                                                                        63 UUUUUGUAUUUAGGUUAGCUAUUUAGCUUU 92
                                                                                                              67 GGTCTAGTCATTCATATAGCTATTTATTTGACCTTTCC 104
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RESULT 6 US-10-995-561-13487/c

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Sequence 13487, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13487
LENGTH: 41309
TYPE: DNA
ORGANISM: Homo Genians
US-11-112-908-65/c ; Sequence 65, Application US/11112908 ; Publication No. US20050260659A1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-24
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US-10-995-561-13487
                                                            RESULT 8
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PRIOR DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
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                                                                                                                        AGGAAGCCCUCUCUGCGGUUU 150
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AGGATGCCTTCTTTAATGGTT 84133
                                                                                                                                                                                                                                              AUUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCC 129
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                                                                                                                                                                                                                                                                                                                                                                      16.3%; Score 30.6; D
27.7%; Pred. No. 28;
ative 33; Mismatches
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29.1%; Pred. No. 16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/102,978
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: PCT/US2003/033152
PRIOR FILING DATE: 2003-10-18
PRIOR PILING DATE: 2002-10-18
PRIOR FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: University of Utah Technology Transfer Office
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
FILE REFERENCE: 0274-5537.1US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
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PRIOR FILLING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILLING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILLING DATE: 2004-11-30
PRIOR FILLING DATE: 2004-11-30
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APPLICANT: Davis, Lisa M.
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 13
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                               NAME/KEY: misc_feature
LOCATION: (80006)..(81089)
OTHER_INFORMATION: Gene VDAC2P; voltage-dependent anion channel isoform 2 pseudogene
                                                                                                                                                                                     FEATURE:
NAME/KY: exon
LOCATION: (56948)...(57115)
OTHER INFORMATION: C21orf34 exon
NAME/KEY: exon
LOCATION: (167308)..(167438)
OTHER INFORMATION: C21orf34 exon
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                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.2%; Score 30.4; 31.9%; Pred. No. 37
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US-10-750-185-47264; Sequence 47264, Application US/10750185; Publication No. US20050260603A1
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, NAME/KEY: exon
; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C210rf34 exon
US-11-102-978-3
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US-10-750-185-32825
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Best Local Similarity 20.0
26; Conservative
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KOSENFELD, David
                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.

APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIN version 3.1
SEQ ID NO 32825
LENGTH: 723
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Publication No. US20050260603A1
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                     APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: BATES, Stephen
APPLICANT: FANTIM, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113138 AAATTCCAATTTTATTGACACAGAATTATCTCAGATTAGCAAAAATAAGTGGTGGTACTT 113197
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                                                                                                                                                                                                                                                                                                                                                                                                637 GTTAACCATAATTACCATGCTTTACATTACA 667
                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AUUUAGGUUAGCUAUUUAGCUUUACGUUCCA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTTTTCTTGTGATGGGAACTTTTAAGACTTAGTAACTTTCAAGTACACATACAGTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.1%; Score 30.2; DB 6; Length 723; 28.6%; Pred. No. 4.4; tive 27; Mismatches 38; Indels
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RESULT 13
US-11-194-246-129
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US-11-194-246-373
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; ORGANISM: Bovine 19866880820089
US-10-750-185-47264
                                                                                                                   Sequence 129, Application US/11194246 Publication No. US20050272089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 373
LENGTH: 2130
APPLICANT: Mott, John
APPLICANT: Mott, John
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND METH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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GENERAL INFORMATION
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Best Local :
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APPLICANT: Mott, John
APPLICANT: Trepod, Catherine
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAB.
TITLE OF INVENTION: USE
TILE REFERENCE: 00592.US1 (M&R 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR PILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/0/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
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PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Sequence of the rpL21 gene and flanking regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: ARTIFICIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                        22 AAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUGUAUUUAGGUUAGC 81
                                                                                                                                                                                                                                                                                                                      82 UAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 16.1%; Score 30.2; D Similarity 31.8%; Pred. No. 6.9;
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5. US20050272089A1
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FILE REFERENCE: 00592.US1 (MGR 268.05920101)
FILE REFERENCE: 00592.US1 (MGR 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
FRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: Patentin version 3.0
SEQ ID NO 129
LENGTH: 2255
TYPE: DNA
ORGANISM: ARTIFICIAL
OTHER INFORMATION: Sequence of the L27 coding sequence and flanking regions.
US-11-194-246-129
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROSENPELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Dennis

ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI11100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: 06/437,482

PRIOR FILING DATE: 2002-12-31

INUMBER OF SEQ ID NOS: 64922

SOCTUARE: PATENTIN VETSION 3.1

SEQ ID NO 57886

LENGTH: 2122
RESULT 15
US-10-750-185-41669
; Sequence 41669, Application US/10750185
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US-10-750-185-57886
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Local Similarity 25.3%; Pred. No. 12;
1e8 22; Conservative 29; Mismatches
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                                                                                                                                                                                                         117 ATCCTGTTTATCTTTCCATTTTTCAGTGGTTCTTAAATAACAATGCTTTGTATAGTAATG 58
                                                                                                                                                                                                                                                    11 AUCUUGCUUGUAAAUACAAUUUUGAGAGGUUAAUAAAUUACAAGUAGUGCUAUUUUUUGUA 70
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                                                                                                                     TCCTAGTTACGTACCTACTTTAAATT 31
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KERR, Richard
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FILE REFERENCE: MMIII00-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOOTWARE: PRICHINI VERSION 3.1
SEQ ID NO 41669
LENGTH: 1228
TYPE DNA
ORGANISM: Bovine 19866881178689
US-10-750-185-41669
Search completed: December Job time : 174.55 secs
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MMI GENOMICS, INC.
                                                                                                                                                             322 TTTTCATTGGCTCAACCATGCAAATTAGCATTATTTTTAGGTTCAAAGACTAAAGCAAAC 381
                                                                                 382 TATACAATGAAAGAAATCCAGAGGCAACCAATTAATTTCCAGGAAG 427
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KERR, Richard
ROSENFELD, David
HOLM, Tom
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DEPINITION Novel tertiary structure having ability to accelerate translation activity.

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WERSTON EXPRODES Triatoma virus

ORGANISM Triatoma virus

Triatoma virus

Triatoma virus

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Dicistroviridae; Cripavirus.

Pristoma virus

Dicistroviridae; Cripavirus.

Novel tertiary structure having ability to accelerate translation activity

Patent: WO 02061080-A 5 08-AUG-2002;

PARAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND FISHERIES, NOBUHIKO NAKASHIMA, VASUSHI KANAMORI PR 25-JAN-2001 PD 10-AUG-2002

PR 25-JAN-2001 PD 10-EVICTOR SENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOWOLOGICAL SCIENCE MINISTRY OF AGRICULTURE PON 2001080-A/5

PD 08-AUG-2002

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PF 31-JAN-2001 WO 2001DF000641

PR 25-JAN-2001 PD 01P 016746

PR 25-JAN-2001 PD 01F000641

PR 25-JAN-2001 PD 01P 016746

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El (bases 1 to 186)

Nakashima,N. and Kanamori,Y.

Novel translational activity-promoting higher-order structure platent: JP 2002306168-A, 5 22-OCT-2002;

Patent: JP 2002306168-A, 5 22-OCT-2002;

Patent: JP 2002306168-A, 5 22-OCT-2002

ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTIC ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES

ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND FISHERIES

OS Triatoma virus

PN JP 2002306168-A/5

PD 22-OCT-2002

PD 22-OCT-2002

PD 22-OCT-2002

PD 22-OCT-2002

PD 100BUHIKO NAKASHIMA, YASUSHI KANAMORI

PC 212N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02// PC
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PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02//
(C12N15/09,C12R1:92),C12N15/00,C12N5/00,(C12N15/00,C12R1:92) CC
Novel translational activity-promoting higher-order structure FFT source 1. .186
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                                                                                                             СААВА ИССАВВЕАСИВИАСАВА ИППИССИА ИАССИСВА В ОСЕВЕНИИ В ОТВЕТЕНИИ В
   UGACUC 186
                                                      CAAGATCCAGGGACTGTACAGAATTTTCCTATACCTCGAGTCGGGTTTGGAATCTAAGGT
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/mol_type="genomic RNA"
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JOURNAL
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Submitted (17-AUG-1999) Centro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence analysis of Triatoma virus shows that it is member of a novel group of insect RNA viruses
J. Gen. Virol. 81 (Pt 4), 1149-1154 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF178440 9010 bp
Triatoma virus nonstructural pro
precursor, genes, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capital
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Scodeller, E.A. and Czibener, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Dicistroviridae; Cripavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10725445
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TGACTC 186
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                                                                                                                                                                                                                                                                                              YCFTEVDYNGSI VGALSYKELVNRICSLYSRRSAFVQSI DSFVTSRFEDLENEEVVAQ
VGYLFGODSKSKVRYLSVA I PSLI ESHVSDMNKRMINLI BKYPET PSNKVI GGVMGLI
AVGLGISTMFWKKTEKKESHVVSFSESCEKVEDRPVVKCESCEKDTQRPTVRCETSTL
DMKVDNQDCDEFLTKSQGVLDLLNASEVLJGKI TKKNLYAMYMGVRLGHAFFI KGCVAS
FPTHF I AAMKLRI SKNPEAEVCFKS PFVNR PVWKMLAKDLI NLSKPFS YKTNLFCDLT
LAPIRVAWSHNDI TDLFVSASEVSRV I ESPAVLPLI MCDNGKDFGVVI KFTSAGSRL
QEKTDLI YKGPDSQNI YLRSAMEYSLDTQSGDCAPLI LRNPMCRGKI CGI HVAGLPT
GGLGTAVPI TKEFILDCLSSFAKHDLTTI CNVPEI SQSGGVSQLPLNEFI TWNDNLST
PGEFGLVGKARA I PSPSKSQ I TESLSHGVI A PVRTRTTLLSP I KTDSGPWNPMHERMR
KYGRPLITALDEELVSTCGAALLNDLASTLARKI DYTNI RSCYDFQTAMSGI DGDETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFNYEPYMNEUCHLOUGHOUGH AND ACHT TO BE AND EACH TO SELLING LAFE CREES.

YFNYEPYMNEUCHLOUGHOUGH AND ACHT TO SELLING LAFE CREES.

I PLAILAPDLKEI LAQSGDQEVPSTDVSINFQQRSDGTYVNFKAQYSGESFSQRI PSTV
EAFCLQHSDLLSRI SEMSPSEFKLVDRYKSRNGEQI VPESQAFSLVEFNLESLQPL

I DQLCSLI SSSISDLFSMEKKYLL QAI VI CVSSLVAVLAYNYL PFRAPSGFCLLI CSLI

I DQLCSLI SSSISDLFSMEKKYLL QAI VI CVSSLVAVLAYNYL PFRAPSGFCLLI CSLI

I PAEDVLCYMREI LDLYI TPQAQSGGI ISSLWFCINVFNALL FRUFKLKSLSEFARFI AI

VPRALQGI DCI GELI SKAFEFARI SFYKYLKSDVFI TQBS PVTKWSGEVQKYYMKYL

SQLVDEI NFNLLGSLY QEGI VMLNSHI FVTARPLI STLLALI SI ILMEFKNRGFSE

STIRNEPYTI YI SGDTGKGSTLSYEPLSADI I KKI AGDTTHDLKNNWKLI YIFRNSEQ

EFWDGYTGQLCCVFDDFGQRI DTSSNENLELFBI I RAANMY PY PLHMABLSQKQNTFF

SSKVLNCSTNVRLEDI KTESLMFPI ALKREPDINVSLKFEI DKESLMKSERFDFSI

VERNYL GARNANDER STRANDER ST
                                                                                                                                                                      NSIKRKSSPGFPWVFKTSSGTGKKQIFGNDGEFLFDTPLAVELEEKVKEVIDLAKQGV
RYSHVFVDALKDERKPREKAHKTRAFSGCPLEYLAVCKMYFQGIVSVLTKCKNETHIS
VGTNVYSKUMDFMARYLKSKSDGFVAGDFEGFDSSQLVPILREIGNVFNGIARQFPDW
YTTEDKREIDVPIRSLDEIAYLKRSFVLDEERQQWIAPLTLDTVLETPSWIHRCDDPI
EATVSNIEFALRELSLHSKQEWEKYAPVMLSEVTRLGRTTIFHDWADTRAFVLDDLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRPSSPLSILVSELEVKFPVFLIRQYNFALDDDKDHWLMTSRQNTGTILDYGYNFGFY
KVPFSEMMYCSCLNCEKTEYDSERVYYENIGEMFDIDPACINGLVIDRYERLRGYPWE
SDKLSYTNSLLDLCLFSSLSERSLQQMFREPRISFEQFSELTLNLGILKPFCRFYSSY
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/note="mechanism of expression unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_id="AAF00472.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="nonstructural
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/db_xref="taxon:103442"
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/mol_type="genomic RNA"
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Argentina
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RESULT 4
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Best Local S
Matches 126
                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                        PUBMED
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                                                                                                                                                                                                                                                    Van Munster, M., Dullemans, A.M., Verbeek, M., Van Den Heuvel, J.F., Clerivet, A. and Van Der Wilk, F. Sequence analysis and genomic organization of Aphid lethal paralysis virus: a new member of the family Dicistroviridae J. Gen. Virol. 83 (Pt 12), 3131-3138 (2002)
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                                                                                                                                     van Munster,M., van den Heuvel,J.F.J.M. and van der Wilk,E. Direct Submission
Submitted (08-AUG-2002) Biointeractions and Plant Health, P
                                                                                                                                                                                                                                                                                                                                                                                       Aphid lethal paralysis virus
Aphid lethal paralysis virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF536531
Aphid lethal paralysis virus,
AF536531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UUGACUC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCA 119
                                                                                                                                                                                                             (bases 1 to 9812)
                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 9812)
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                                                                                                                                                                                                                                                  Virol.
                                                                                                                 International,
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ADGVDGLPLSLKYGNEVILKFPAGTSSDEVALEYVLKI PNIFSRFKYSSTSLFKQV
LMTSPVHPQI IRNHYTVUDAFGQFTLLAYATGFFKYNRGGLVYTFRFVKTVNISGRVQ
ITFHPFVGYDDVMDSDGKI VRDEYVRVVDLTRDTFSLTFVFXVCADVFN
SANRFVGYDDVMDSDGKI VRDEYVRVVDLTRDTFATLVVPFTSLTFYKVCADVFN
SANRFVGYDERFTSTERFSLGVFIACVGFLFVSSSAVVSSTI DVLVEVKASD
DFELAVFNTPLMLFVDSLTERFSLGVFIACVGFASAGTRDI RSSYVBGKFI FQDITG
MSRNHELDEQPSQECIGERILSFSELI KRNSWRYVSDEKSLI YPAYAFDNPAAMYTAA
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GYIIKANDYSTDFCSSNIYENFYTKGIAEVQTPYYSRVNTSVVSAPVLYNAGNISPLM
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ttfvhloriiteqligdsqpsgdvrsysdarthsiidflerpcggrlvlavyvpglik
Keifeslkledalmsemifekligftsgrsattvhiqvnahefpcggrlvlavyvpglip
plhrlumlsfdvsnvitlehvqldisketevllkipyvsffvqydlvtkftpwaafla
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/product="capsid protein precursor"
/protein id="AAF00473.1"
/db_xref="GI:6003486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNVMYKITSNSSNILLGHSAADDFRFGFLLGAPLAISATALRDNFTGSSATVSLPTFS
organism="Aphid lethal paralysis virus"
/mol_type="genomic RNA"
                                                                   Location/Qualifiers
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Pred. No. 2.9e-42;
0; Mismatches 0; Indels 1
                                                                                                                 Biointeractions and Plant Health, P.O Box 16, Wageningen 6700 AA, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9812 bp
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19 UUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGUUAAGGUUGCGCUUG 78

Matches Query Match Best Local

Similarity

19.8%;

; Pred. No. 2.9; 23; Mismatches Score 36.8; Pred. No. 2.

Indels Length 9812;

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DB 13; 47;

Conservative

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ORIGIN
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YEPBDI VEHPIDAEAQIGNAARVAAGNVAGELVTNIHCLRKYVHGDDDTILMALLRKTK
RTMENI LDYTGLI PRAEDI WEDPSWDYHLYXARQI KQYLKDASTGI METLAGFEKYW
QFVKQAVLUGVSVFSTYMCUKVSFALGDYVKGKI VPKYI SDNDQVAQLUVSEANACFDK
GCNNCKLCKNAAMNQLNVKMNSGLLCYVKRMEKGKDMINKYA I SLYGDQRVSNNHELS
VDMABI I NQVADCDONTCDCCNDPELLDRLSTVAR I HGTNCVLLTRFYQGFKTADL
VDMTKQI SNTLESI I KVPELKKLI DSHAFVYNAV SRRANSTRI VGHGATYDARPRTR
MVTKIGAQAVYDNRVTI KXWTI LAAQNLLPAFAKI BPI EKTMDI QYVDARFATRI FOR PITAGREGMI
PKHFLYVMEHYVETFGSENCHFVLENCSNA I SPLI PGSVI LEQENHVKDPRRDI A VO
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AQIDTGSHLLILKALSITMFCLFIKQLPGKVTIDEFVTRLDEFPKAISGLESMWSKLD
VVVKQIYTFWEEILKKGHRENNTDLM-DQVLDMASEVEKYLELANURIE KRDDATVLAA
SKLYPRGVRLIKECTQLKLSPANLMLIRSLLPATKQLADBAIKSGALKQALREPLIIV
WFCGKSGMGKTGMSYFFMMDMRVFGDIPTDCKNIYGRVPETFYMDGYTDQBIIYIX
DAFQIKONULKENPELFEIIHGUNAFPVMLHASVEEKNMFPANPKCYLLTSNLDIIYK
TESLNSPEAVQRRIDFAYNVDIAEEYREYYYDQNGNEKYKLNAVKARAARKLVGTSV
                                                                                                                                                                               SNYARPALMVSNTIRDVAKHEGÄSKRTTABÄPHLNKLTGSREMANADGVDMSHSIGIS
AINBLEVRALMTRIDIDEMTVAHIARIPCIRKERAMTSNIGKAGDULYATPITPSFFSI
AVBSTRVAPSHLAYISSFPTIMMRGGINEHEKEVKTKEHSGRVRILFVPGDYSNDDKLP
DNADENASYSSVVDLRSDTDVTENVPFVSVQPMKLSSADVTSPLKDYQHSVGRLYVLI
LNELGATSTVSDTISCLVEVSGASDFELSMERQPKIFTLRAKSTTLNRVIRGIAQV
NVARSTPVSPEIJOKTGGEVGESSMRQPQGTSFTSSALTVGEKVTSLAQILKREHLISS
NVATSTBVSDTINSFKTPKPIAQATMVNIDLYSYYSYIFAYYRGSFREKIAPEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="panfqetqmtheqqqiltfessegmtestsiytdplldmsylts
vddgrhhsiidflqreiniqwiesgtmangktlmavdleldei innswykaktes
geradvelkklqvnaqefqagrlllvyifgykyigetgerkyvddrtnvddaslveltges
prvdldlstctbatmcvpyxspylfsdltngvgtigerkvvvvsplvdgassgivDct
lminfknikikyptampiaataqvgteaiqdsagagvissaaasvssylsplqdvply
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TPEDHILVESTYVEBANVVQNRGSYTYHAVTFFGDCGSILIASNAAITQKIMGMIAGI
THMMKGISVALTRQIIDRLAMKHQPJEYSQYGHEIVPLDVNPDILKENGTFLIYGTELGR
RIMGSVKTALEKSPAYGKLIESPNKPGYLRPFTDENGTTIDPMTLQRNKYGVVRPYVS
QQRVDAVYBANSVFYQREYINSPAHYKLPLTREETIVGINGDPINALNRQTPAGYPY
TYEKEGKSGKTKWFGCDGMYVDLTNDACKQLMADVDBLAQCHLDNVRPRIINIOTIKLDA
KIPIAKANVGKTRLFTACPLHYTILFRQYFLPFIAHAMRNRVQNSIAVGINPMSPEMD
                                                                                  KVYAAR IRL I PENGATEANAGPVQEDNTVI DETRTAADVYMPRNLEGTFEFQVPHYSR
YPLLPNTAGS I PVI GVQDLI QRNLVSVNI LTEAETTKALFYRAVGDDFS FCGLLGPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="encodes CP1, CP2 and CP3; start codon not
determined"
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TLYINKLSAIAQVGLNFNHNITVDNNLELAINKSLTMFADLTNAISDKLQETVADYQR
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/protein id="AAN61470.1"
/db_xref="GI:24431319"
/translation="MSGTFSTTLPQLKLQLSIPELTQLKIRDAQAHEKPRIVAQLTRS
TLENMNNTXIMTEPLDAIPENTLRKQVLAXITEFNESHNGVSRPSRIAQLDGNIAXIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="capsid protein precursor"
/protein_id="AAN61471.1"
/db_xref="GI:24431320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIGNQLPLRICVDTLSGGLTELAMHDKVTDAKWRTKMINLGLDLTRGTGLEFNPDSRS
TTLLKLRNEELGGDFEINY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHCCLADSWLDIMDGTPYATMNSFFEHTSSIFYGDDFIMNIRPEVIDVYNQETLTPVL
KKNLEMTMTDEAKTGECVKARTLEEVSFLKRKFRFESFVGLWVAPIDIDVILDAPNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELDYDEFEQFLMKIGVECINHLHIANHSDLTGAALIYYVRNGIPSGCPATAILNSIV
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/protein_id="AAN61470.1"
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RESULT 6
BD173513
LOCUS
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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SOURCE
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AX763949
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PATENT AND ENGLANCE PER 31-JAN-2001 WO 2001JP000641

PATENT STANDARD AND STANDARD STANDARD AND S
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TITLE
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Best Local Similarity
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WO 02061080-A/3.
Drosophila C virus
Drosophila C virus
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Nucleic acid derived from an ALPV virus,
said nucleic acid and uses thereof
Patent: WO 03040177-A 1 15-MAY-2003;
Plant Research International B.V. (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity.
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Aphid lethal paralysis virus
Viruses; saRNA positive-strand viruses,
Dicistroviridae; Cripavirus.
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Sequence 1 from Patent WO03040177.
AX763949
AX763949.1 GI:32258304
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/mol_type="unassigned RNA"
/db_xref="taxon:209529"
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37.5%; Pred. No. 2.9;
vative 23; Mismatches
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having
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BD177017
LOCUS
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PF 25-JAN-2001 JP 2001016746
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Novel translational activity-promoting higher-order structure FH
C12N15/09, C12N15/00, C12N15/00, C12N15/00, C12R1:92) CC
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Nakashima, N. and Kanamori, Y.
Novel translational activity-promoting higher-order structure Patent: JP 2002306168-A 3 22-0CT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         578 TATTITAATAATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCTATTGGCAGCCCC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                   638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1345 bp DNA
Sequence 1072 from patent US 6703491.
AR496112
                                                                                                                                                                                                                                                                                  AR511394 1345 bp DNA
Sequence 16354 from patent US 6703491.
AR511394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila sequences
Patent: US 6703491-A 1072 09-MAR-2004;
Exelixis, Inc.; South San Francisco, C
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1345)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L.,
Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
                                                                                                                         Drosophila sequences
Patent: US 6703491-A 16354 09-MAR-2004;
Exelixis, Inc.; South San Francisco, CA
                                                                                                                                                                  1 (bases 1 to 1345)
Homburger, S.A., Ebens, A.J.
Margolis, J.S., Reddy, B.P.,
                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                      AR511394.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
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                                                                                                                                                                                                              Unclassified.
                                                                                                                                                                                                                                         Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                   ATAATATCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                Location/Qualifiers
1. .1345
                                                                    /organism="unknown"
/mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="unknown"
                                                                                                                                                                                                                                                                     GI:52446869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 36.4; D: 38.6%; Pred. No. 4.5; Live 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   649
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                                                                                                                                                                  Ebens, A.J. Jr., Erickson, C.S., Reddy, B.P., Ruddy, D.A. and Buch
 Score 36.4; D
Pred. No. 4.5;
28; Mismatches
                                                                      DNA"
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                          DB 6;
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  51;
                           Length 1345;
                                                                                                                                                                       Buchman, A.R
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  Indels
                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                  Francis-Lang, H.L.,
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  Gaps
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ORGANISM
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VERSION
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DEFINITION
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AF014388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The novel genome organization of the insect Drosophila C virus suggests this virus belon undescribed virus family Gen. Virol. 79 (Pt 1), 191-203 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila C virus strain EB, complete genome. AF014388
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Drosophila C virus
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1 (bases 1 to 9264)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 9264)
Johnson, K.N. and Christian, P.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson, K.N. and Christian, P.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses,
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                                                        KDGVGSEQMMGNLTRICDFLENTLPGILQANIQATVIDTTDKYVSIKEDIMKIVLVILL
VRLLMVWKKKRASLCVILIFIFKYGFDQKLIDLIMDLKKKIFSQGALEDTVEEVYH
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SGVGKTEMVYPLCIDVLREMGMIKKDDFHHQVYGRQVETTEFWDGYKGQKIVIVDDAFQ
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IVRDEKSDAGWIDSGSPLDYEDFAKLVCSKWEAKQSSMNKLKFLEETAIFAVQKSE
NSEYGGCIDFVDDIAKRLQKGSTLEBIEFDYASDPEMFTQYYHKKSTIKPASRWQKYK
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VGQSGDVKTMKAQIKRVEAGABELVTVAALTGCCSDDAAHNLMIDVFQKRTYRMSYFRG
                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="mesdksmaclnrilmnkmmfvedkistlkmvadyyokevkydfd
avespreapvfrctcrflgytimtogigkknpkoeaaromllllsgdvetnpgpvosr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="includes putative protease, helicase and
domains; putative; ORF-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (16-JUL-1997) Entomology, ACT 2602, Australia
SGAMATFHVNNMGLYRVYNWLNAVRÞCDKKIEIFHÞEDGFEYÞEESYIQRDCYEYNAÞ
                      DKRYQLGNCTFVRGMSFIMPYHFVQAVFARRLÞÞNTIISLSQQMSEDLMQIÞLSHFFS
AGVDNFYLTDNCVRLÞFKNGDFRDCVMVNLHSRMCTÞHRDLVRHFILTSDQGKLKGSF
                                                                                                                                                                                                                                                                                                                                                                                                  PVYYRYNDPRYTRLEKAIERRDDKIKTLIKELRRQIKNRKIYSQGMFDKLTKQISDGI
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/product="replicase_polyprotein"
/protein_id="AAC58807.1"
/db_xref="GI:2388673"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic RNA"
/strain="EB"
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                                                                                                                                         Hominidae, Homo.

Hominidae, Homo.

1 (bases 1 to 128544)

1 (bases 1 to 128544)

Polley,A., Baumgart,C., Blechschmidt,K., Dette,M.D., Jahn, Polley,A., Reichwald,K., Schilhabel,M.B., Schudy,A., Taudi
Menzel,U., Reichwald,K., Schilhabel,M.B., McCray,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51,
2 (bases 1 to 128544)
Schudy,A., Schilhabel,M., Schutte,B., Ganz,T., Linzmei
Ho,C.H., Hoang,B.V., McCray,P., Baumgart,C., Menzel,U
                                                                                                                    Chromosome 8
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF238378 128544 bp DNA linear PF Homo sapiens chromosome 8 clone SCb-561b17 map p23.1,
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                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AF238378.5
HTG.
                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
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ilarity 38.6%;
Conservative :
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TVWAHLEDVDVQYETGANIFTGSSENRASLGQRMSDGKFEKDLRDLWTSKANKQPD
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IVAVAPQGTIATTDVVNAQFARAPSDDFSFMYLVGVPPLTNVARP"
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WTHSQDESGNPFTVIINCLYNGIIMRLSWIRVMEKFQPBLKSMKMFNEYVALITYGDDN
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LQRHVAPLKIEVIYEMLNWSRRSIDPDEILMSNIETAFREVVYHGKEEYDKLRSAVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKVPQELPENPQILTYNQYLHDIEYLADPLYDF"
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                                                                                                                    8 genomic sequence
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Pred. No. 3.9;
28; Mismatches
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                             Linzmeier, R.,
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                                                                                                                                                                                             Jahn, N.,
Taudien, S.,
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Submitted (08-JUL-2004) Genome Analysis, Institute of Biotechnology, Beutenbergstr. 11, Jena 07745, Germany 9 (bases 1 to 128544)
Lagemann, D. and Platzer, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-AUG-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena 07745, Germany On Apr 2, 2003 this sequence version replaced gi:21700555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biotechnology, Beutenbergstr. 11,
8 (bases 1 to 128544)
Lagemann, D. and Platzer, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biotechnology, Beutenberstr.
7 (bases 1 to 128544)
Lagemann,D. and Platzer,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-APR-2003) Genome Analysis, Institute of Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotechnology, Beutenberstr.
6 (bases 1 to 12854)
Lagemann,D. and Platzer,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-JUL-2002) Genome Analysis, Institute of Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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Lagemann, D. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-NOV-2000) Genome Analysis, Institute of Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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Submitted (22-FEB-2000) Genome Analysis, Institute of Molecular
Submitted (22-FEB-2000) Genome Analysis, Institute of Molecular
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                   Sequencing vector: DUCL8; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 127999 bases at least Q30 (Consensus quality: 128330 bases at least Q30 (Consensus quality: 128344 bases at least Q20)
                                                                                                                                                                                                                                                                                          Web site: http://genome.imb-jena.de/Contact: gscj-submit@genome.imb-jena.de
Quality coverage:
                                                                                                                                                                                                                                    Center project name: H370
Center clone name: SCb-561b17
                                                                                                                                                                                                                                                                                                                                                                                         Center: Institute of Molecular Biotechnology Center code: IMB
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11.05x
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. quality >=

Neighboring sequence information:

This clone is overlapped by SCb-540n10, SCb-332a23, CTB-415D8

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.

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FEATURES
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polyA_signal
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Base-by-base quality values are not generally visible from GenBank flat file format but are available as part of this entry's ASN.1 file.
                  /note="MLT1G1 repeat: matches 490.

complement (10067. .10240)

/note="MRR67D repeat: matches 335.

complement (11088. .11093)
                                                                                                                                                                        8067. .8429
/note="MLTIA0 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                /translation="MRTLAILAAILLVALQAQAEPLQARADEVAAAPEQIAADIPEVV
VSLAWDESLAPKHPGSRKNMACYCRIPACIAGERRYGTCIYQGRLMAFCC"
complement(2216. .2340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1562. .1567)
/gene="Em:AF200455.12"
complement (join(1668. .1777,2358. .2532))
/gene="Em:AF200455.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="novel protein, similar to DEFA1" complement(join(1547. .1777,2358. .2544,3904. .3983)) /gene="Em.AF200455.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2971.
complement(1547. .3983)
/gene="Em:AF200455.12"
                                                                                                                                                          8430. .8478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="continues in clone Em:AF200455.12
protein match: Tr:Q9TTZ9 Tr:Q9TU00"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="defensin, alpha 1, myeloid-related sequence"
/note="continues in clone Em:AF200455.12
cDNA match: Em:BC027917.1 Em:X52053.1 Em:M21130.1
Em:AF184159.1 Em:AF184160.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="overlapping clone" complement (227. .526)
      complement(11290. .12157)
                                                                                                                                                                                                                                               7944. .8066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST match: Em:BU615878.1 Em:BQ182900.1 Em:BQ446731.1"
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="defensin, alpha 1, myeloid-related sequence"
/protein_id="AAT68883.1"
/db_xref="GI:50057847"
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                                                                                                                                                                                                                                                                note="Ll repeat: matches 4948. .5358 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Em:AF200455.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="CTB-415D8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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|mol_type="genomic DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
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                                                                                                                                   'note="MLT1G3 repeat: matches 161.
                                                                                                                                                                                                                        note="MLT1G3 repeat: matches 37. .162 of consensus"
                                                                                                                                                                                                                                                                                                              note="MIR3 repeat: matches 4. .144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="overlapping clone"
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lone="SCb-332a23"
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                                                                                         .587 of consensus"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CAAGAUCCAGGGACUGUACAGAAUUUUUCCUAUACCUCGAGUCGGGUUUGGAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 UAGUUAAGGUUGCGCUUGCCUAUUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 UUGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUA
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                                                                                              The genome sequence of Canis 
Unpublished (2004)
                                                                                                                                                                                                                                         Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                               S237P6298FG12.TO PortugueseWaterDog
                                 Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biome
                                                                                                                                      1 (bases 1 to 636)
Lindblad-Toh, K.
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                    BV432331.1 GI:57850264
                                                                                                                                                                                                                                                                                                                                        sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                      BV432331
320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 26.2
15; Conservative
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/note="L2 repeat: matches 2971. .3294 of consensus"
complement (20650. .23086)
/gene="Em:AF200455.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER41A repeat: matches 395. .468
complement(11820. .11904)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="novel protein, similar to DEFA1"
complement(join(20650. .20880,21461. .21647,23007. .23086))
/gene="mm.RF200455.14"
/product="defensin, alpha 1, myeloid-related sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg repeat: matches 10. .310 of consensus"
complement(18218. .18519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MLT1A0 repeat: matches 132. .372 of consensus"
complement(17266. .17568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (17266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1P4 repeat: matches 5267.
16126. .16358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MBR54B repeat: matches 341. .476 15608. .16125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1 repeat: matches 4955. .5360 of consensus"
13476. .13615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MIR3 repeat: matches 82.
12866. .13279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (11736. .11806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="defensin-related pseudogene
continues in clone Em:AF200455.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (11290. .12157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER67D repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="DEFT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="defensin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="DEFT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="defensin, theta 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.4%; Score 36; DB 8; Length 128544; 26.2%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                        for Biomedical Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  636 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 theta 1"
                                                                                                                     familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matches 194.
                                                                                                                                                                                                                                                                                                                                                               DNA linear STS 02-FEB-2005
Canis familiaris STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5789 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .514 of consensus"
                                        Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of consensus"
                                          for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 13 AC137051/c LOCUS DEFINITION

REFERENCE

AUTHORS

KEYWORDS VERSION ACCESSION

ORGANISM

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STS
ORIGIN
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                       129
62 AGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUC 96
                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                         2 исаспансиссинссиниссинанальнай специальная поставления в 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WGS reads. Since this sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poddle sequence was placed uniquely on the CanFamiloboxer assembly and SNP boxer assembly as a sequence of the boxer assembly as a sequence of the boxer as a sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the ten flanking the bases. For each allele, at least one additional read had to bases. For each allele, at least one additional read had to it. 731476 SNPs were annotated with alleles between the two boxer alleles. The validation rate for these SNPs was estimated at approximately TBD%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%.

Internal-WGA-discovery (I-WGA):
A third set of SNPs were discovered by comparing reads in the WGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         defined as mismatch positions that had a base quality of >=30 on both reads in a region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs:

A second set of SNPs was generated using a similar methodology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that aligned without gaps, and with at most one additional mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which the particular read came. The validation rate for these SNPs was estimated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotated with alleles from the boxer and the breed or canid from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Water Dog -100,000 each)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retriever, English
Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from the 1.5x poodle assembly (Kirkness 2003) were used instead of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      except that the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485941 SNPs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Californian Coyote).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wolf as well as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paired-end low-coverage whole genome shotgun reads were generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer A: No sequence submitted
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from 9 breeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGS-discovery (WGS):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
                                                                                                 TGACTGTGAGGCCTTGGTTTGTAAGGATTCTCTGAGCCCCAGTTTGTCATGTGTTGCTAT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGS reads were placed uniquely on the Canfaml.0 boxer assembly SNP detection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           five other canids (Chinese, Alaskan, Indian and Spanish Gray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             size: 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kersli@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="PortugueseWaterDog"
/db_xref="taxon:9615"
/map="+ Un 22-582 54898954-54898394"
/clone_lib="PortugueseWaterDog"
<1. .>636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Canis familiaris"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNPs were
                                                                                                                                                                                                                                                                                                                                               19.2%;
                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                               Score 35.8;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                             Length 636;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                           Gaps
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sequence in this assembly is a combination of BAC based reads

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Allen, C., Allen, H., Alabrooks, S., Amin, A., Angulano, C., Alden, W., Aloys, C., Allen, H., Alabrooks, S., Amin, A., Angulano, D., Ander, J., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balwalo, K., Balden, H., Baca, E., Baden, H., Balwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Balwende, F., Blawelo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Cater, Dederich, D., Devida, M., Davis, C., Davy-Carvoll, D., De Anda, C., Dederich, D., Delgado, O., Denson, S., Dermo, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claveland, C., Cockeell, R., Cox, C., Coyle, M., Gree, A., D'Souza, I., Casar, H., Chen, Y., Chen, Z., Chu, J., Chen, S., Denn, A., Durbin, K., Duval, B., Baves, K., Draper, H., Davis, C., Deverson, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, S., Denn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Espere, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagy, M., Forbes, L., Foster, M., Foster, P., Ferrandez, S., Denn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Espere, C., Brans, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Gebrerg, W., Gill, R., Grady, M., Gorera, W., Gevara, W., Gellin, B., Howells, S., Huly, K., London, P., Lowes, D., Jolkson, A., Jackson, A., Harvey, Y., Havlak, P., Havlak, B., Hawes, A., Henderson, N., Hernandez, J., Liu, J., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, W., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, W.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Depar
Submitted (14-NOV-2002) Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239102 bp DNA linear F Rattus norvegicus clone CH230-unknown, WORKING DRAFT unordered pieces.
                                                                                                                                                    Rat Genome Sequencing
                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS PHASE1;
                                                                                                                                                                                            (bases 1 to 239102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 239102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:25007182
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                                                                                                                                                            Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG 15-NOV-2002
T SEQUENCE, 2
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AC137461/c
                                                                                              RESULT 14
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   DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               47807 TITACITIGGCITGTITCATICITAATAATICACICATICAAAGACCAAAGTAIGGICA 47748
                                                                                                                                                                                                                                                    61 UAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCA 99
AC137461 267809 bp DNA linear HTG 20-NOV-2002 Rattus norvegicus clone CH230-unknown, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                         1 UUGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                          TAGTGAATCATTCTCTGGGCAATACACTATACTTCCTCA 47709
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------ Summary Statistics
Assembly program: Phrap; version 0.990329

Consensus quality: 225198 bases at least Q40

Consensus quality: 227434 bases at least Q20

Consensus quality: 228930 bases at least Q20

Estimated insert size: 230911; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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91380. .93878
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58818. .60157
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58718. .58817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="wgs_contig"
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_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.8%; Score 35; DB 14; Length 239102; 36.4%; Pred. No. 7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eryant, M., Bulay, C., Bulkel, F., Bulkel, R., Cardenas, C., Cardenas, V., Charter, K., Chen, E., Chen, E., Chen, C., Chen, C.
                     Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') Within each contig-scaffold.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroida; Muridae; Murinae; Rattus.
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individual sequence contigs are ordered and oriented, and separated
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NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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265370
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Center code: BO
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                    /note="wgs_contig"
265270. .265369
                                                                                                                                                                                                                  /note="wgs_contig"
142596. .143821
                                                                                               /note="wgs_contig"
211046. .212894
                                                                                                                                         180964.
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108632. .110236
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16011. .17501
                                                                                                                                     /note="wgs_contig"
180964. .182519
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146719. .147808
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1. .267809
  estimated
                                                          /note="wgs_contig"
246154. .247283
                                                                                                                                                                                                                                                         /note="wgs_contig"
L30438. .131667
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123509. .124765
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20015. .21050
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|5100. .96591
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_xref="taxon:10116"
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9. .52759
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                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPBE; Information on the WORMPEE database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the their face of the monomucleotide A/T runs and conserved TA repeats. Where
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discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, Washb). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-96H14 is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Sep 17, 2004_this sequence version replaced gi:52213928.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 UUGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUA
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Zebrafish DNA sequence
                                                                                                                                                        Repeat names beginning 'Dr' were identified by the Recon repeat
                                                                                                                                                                                                                      this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
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(bases 1 to 126572)
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| ABA58832 AAI38538 AAK32723 | AAS46376 ABL32823 AAZ08975 ACN44728 ADK53988 ADK53988 | ABZ80711 AAL50548 AAL60324 ABZ80709 ABZ80710 AAL50546 ABZ80710 AAL50547 ABQ33052 ABT22167 | ID |
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| ADA70696 ADJ39578 ABL34125 | ADG62976 1 ADZ46976 1 ABN85733 AAV87077 ADX65104 | AAH17724 ABL18096 AAD49503 ADL33372 ABS57422 | AAL280708 AAL50545 ACH44858 ACH411148 AAH111148 ACA03978 AAQ10896 AAS29606 | AAK06986 ABS32442 ABS07519 ABV46608 AAL24946 ABK75374 |
| Ada70696 Rice gene Adj39578 Plant cDN Abl34125 Human imm | Adges9/4 Human pro Continuation (2 of Abn85733 Mouse gen Aav87077 EST clone Adx65104 Plant ful | Aah17724 Human CDN Ab118096 Drosophil Aad49503 Human TRI Add133372 Human tra Abs57422 Human pro | | |

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RESULT 1
ABZ80711
ID ABZ8
AC ABZ8
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Pseudoknot; secondary structure; cell-free protein synthesis; albumen; impurity; higher-order structure; intergenic region; internal ribosome entry site; ss. wheatgerm; IGR-IRES;

WO2003033719-A1. Triatoma virus.

08-OCT-2002; 2002WO-JP010447.

24-APR-2003.

17-OCT-2001; 2001JP-00319923.

(NAAG-) NAT INST AGROBIOLOGICAL SCI. (WAKE-) WAKENYAKU KK.

Nakashima N, Shibuya N, Nishikawa S;

WPI; 2003-403230/38.

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

Claim 1; Page 33; 39pp; Japanese.

The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

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RESULT 2
AAL50548
ID AAL5
XX AAL5
XX AAL5
XX AAL5
XX AAL5
XX AAL5
XX CrPV
KW Grug
KW Grug
XX WO20
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XX WPI,
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Matches 186;
                 The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing are producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene
                                                                                                                                   Claim 1; Fig 1-2; 38pp; Japanese
                                                                                                                                                                               Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                                                                                                                                                                       WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;
                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001; 2001JP-00016746.
                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2001; 2001WO-JP000641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              higher-order sequence from the Triatoma virus. The sequence is use construct which may also include an intergenic region and internal ribosome entry site (IGR-IRBS). The method is applicable in produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 186 BP; 49 A; 35 C;
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   technique.
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Pred. No. 1.1e-54;
; Mismatches 0;
     nucleotide
     represents
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     Triatoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is used in
                                                                                                                                                                                    application
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                   gene
                                                  and
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Query Match Best Local

Similarity

19.8%;

Score Pred.

36.8; DB No. 0.093;

Length 9829

Sequence

9829

B₽;

3083 A; 1906 C; 1879 G;

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2961

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Best Local
                              The invention relates to a novel RNA derived from an ALPV (Aphid lethal paralysis virus). ALPV RNA is useful for controlling homopterous insects such as aphids or white files. It is useful in the research concerning aphids and for controlling aphids and in the field of agriculture or floriculture. It is also useful for detecting ALPV- viruses using PCR and for preparing a monoclonal antibody against antigen which is synthesised in vitro. The invention is also useful in gene therapy. The present
                                                                                                                                                                                                                                                                                                                                                                        Aphid
                                                                                                                                Claim 1;
                                                                                                                                                                               Novel
                                                                                                                                                                                                                              Van Der Wilk F,
                                                                                                                                                                 detecting
                                                                                                                                                                                                                                                                           25-OCT-2001; 2001NL-01019225
                                                                                                                                                                                                                                                                                                   25-OCT-2002; 2002WO-NL000682.
                                                                                                                                                                                                                                                                                                                           15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                  WO2003040177-A2
                                                                                                                                                                                                                                                                                                                                                                                                             ALPV;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Aphid lethal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL60324;
                                                                                                                                                                                                                                                      (PLAN-) PLANT RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAL60324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA sequence of the
                                                                                                                                                   . nucleic acid derived from aphid lethal paralysis virus, useful ting ALPV-viruses, for preparing a monoclonal antibody against pen, in research concerning aphids and for controlling aphids.
                                                                                                                                                                                                      2003-441523/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                             Aphid lethal paralysis virus; white fly; agriculture; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                        lethal paralysis virus
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                                                                                                                               Page
                      is ALPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGAUCCAGGGACUGUACAGAAUUUUCCCUAUACCUCGAGUCGGGUUUGGAAUCUAAGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UGACUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UUGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UGACUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGAUCCAGGGACUGUACAGAAUUUUUCCUAUACCUCGAGUCGGGUUUUGGAAUCUAAGGU
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                                                                                                                                                                                                                                                                                                                                                                                                                                   paralysis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                               10-13; 17pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                              Van Munster
                        RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 A; 36 C; 44 G; 0 T; 64 U; 0
                                                                                                                                                                                                                                                      INT BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             homopterous insect; floriculture; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA.
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Best Local S
Matches 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Drosophila C virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                             Sequence 189 BP; 57 A; 30 C; 34 G; 0 T; 68 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 32; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001; 2001JP-00319923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     albumen; impurity; highe internal ribosome entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudoknot; secondary structure; cell-free protein synthesis; wheatgerm; albumen; impurity; higher-order structure; intergenic region; IGR-IRES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ80709 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NAAG-) NAT INST AGROBIOLOGICAL (WAKE-) WAKENYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6716 GUUAUUUAACUUUACUUAUCAAGAUGGCCGUUGGCAGCCCCACGAAAUCUAG 6767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-403230/38
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                                                                                                                                                                                                                                                              l Similarity
79; Conserv
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                           UAUCUUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCC
                                                                               AUAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCA 119
                                                                                                                                                                        UGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCU---
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                                                                                                                                                C virus derived pseudoknot sequence
                                                                                                                                                                                                                                                           19.6%;
ilarity 59.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                       Score 36.4; DB Pred. No. 0.027;
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                                                                                                                                                                                                                                                                                                                   DB 8;
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                                                                                                                                                                                                                                                                                                                   Length 189;
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                                                                                                                                                                                                                                                              Gaps
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AAL50546
ID AAL5
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RESULT 6
ABZ80710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local (
   ABZ80710 standard; RNA; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-627482/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakashima N,
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                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAAGAUCCAGG 131
                                                                                                                                                                                                          ACAAGAUCCAGG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUAAUAUCCAGG
                                                                                                                                                AUAAUAUCCAGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kanamori
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The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Drosophila C virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CrPV-like virus; ss; higher-order structure; drug drug production; translational activity-promoting
                                                                                                                                                                                                                                                                                                                                                            Sequence 201 BP; 61 A; 33 C; 35 G; 0 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein synthesis; structural analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NAAG-) NAT INST AGROBIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001JP-00016746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila C virus RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL50546 standard; RNA; 201
                                                                                                                                                      UGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCU---
UAUCUUAAUAAUUAGGUUAACUAUUUAGUUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCC
                                                        AUAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCA 119
                                                                                                                    2001WO-JP000641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                 19.6%;
                                                                                                                                                                                                                                        Score 36.4; D
Pred. No. 0.02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               72 U; 0 Other;
                                                                                                                                                                                                                                                                       .028;
                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development;
function;
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      121
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BP

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AALSOS47
AALSOS47
ID AAL5
XX AAL5
AC AAL5
XC AAL5
XX TJ-D
XX TJ-D
XX CrPV
XW CrPV
XW drug
XW prot
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                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
 CrPV-like virus; ss; higher-order structure; drug drug production; translational activity-promoting protein synthesis; structural analysis.
                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Cricket paralysis virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in
                                                   Cricket paralysis virus RNA sequence
                                                                                 19-DEC-2002
                                                                                                                                    AAL50547
                                                                                                                                                                                                                                                                                                                                                             Sequence 188 BP; 56 A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                       producing useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 33; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002; 2002WO-JP010447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cricket paralysis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-403230/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2001; 2001JP-00319923.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudoknot; secondary structure; cell-free albumen; impurity; higher-order structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ80710;
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                                                                                                                                                                                                      131
                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAT INST AGROBIOLOGICAL SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 paralysis virus
                                                                                                                                    standard;
                                                                                                                                                                                                                                                                      UUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGAUCCA
                                                                                                                                                                                                     GGAA 134
                                                                                                                                                                                                                              GGGA 133
                                                                                                                                                                                                                                                     UUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosome
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibuya N,
                                                                                                                                                                                                                                                                                                                                                                                       proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry
                                                                                                                                    RNA;
                                                                                                                                                                                                                                                                                                                       18.1%;
70.3%;
                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived pseudoknot sequence
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                                                                                                                                    ВÞ
                                                                                                                                                                                                                                                                                                         o,
                                                                                                                                                                                                                                                                                                         Score 33.6; D
Pred. No. 0.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             36 G; 0 T; 63 U;
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                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein synthesis; wheatgerm;
intergenic region; IGR-IRES;
                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                             Other;
                                                                                                                                                                                                                                                                                                                                  Length
             development;
function;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                        0
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RESULT 8
ABQ33052
ID ABQ3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                        Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
01-SEP-2000;
05-SEP-2000;
                                      01-SEP-2001; 2001WO-EP010074.
                                                                07-MAR-2002
                                                                                                                   Homo sapiens.
                                                                                                                                                                                                               Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                have a higher-order structure that sustains translational activity-
promoting function. The RNA sequences of the invention are useful in the
synthesis of proteins and polypeptides for application in developing and
producing drugs. The RNA sequences of the invention are also useful in
basic research of protein synthesis and structural analysis by the gene
recombinant technique. The present nucleotide represents a Cricket
paralysis virus RNA sequence of the invention
                                                                                                                                                                                                                                         12-JUL-2002
                                                                                                                                                                                                                                                                                            ABQ33052 standard; DNA; 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 200 BP; 60 A; 36 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises seven RNA sequences (CrPV-like viruses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NAAG-) NAT INST AGROBIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JAN-2001; 2001JP-00016746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cricket paralysis virus.
                                                                                                                                              cell differentiation; ds
                                                                                                                                                                                                                                                                                                                                                              131
                                                                                                                                                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                      70 UUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGAUCCA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                              GGAA 134
                                                                                                                                                                                                                                                                                                                                                                                        GGGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                UUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
2000DE-01043826
2000DE-01044543
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-JP000641
                                                                                                                                                                                                             for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.6; D
Pred. No. 0.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 G; O T; 67 U; O
                                                                                                                                                                                                             cytosine methylation SEQ ID NO 19643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 26 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 9
ABQ33053/c
ID ABQ330
XX ABQ330
XX 12-JUL
XX Oligon
DX Oligon
XX Grey
EW Human;
KW Human;
KW Grug;
KW G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          र्
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CD DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on CC the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used: CC oligomers, the degree of diseases, e.g. cancer, disorders of the central CC or disgnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for CC investigating cell differentiation. The method allows the methylation CC status of many C residues to be determined simultaneously. ABQ13410-CC ABQ54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphi SNP; cell differentiation; ds.
   01-SEP-2000; 2000DE-01043826.
                                                                    01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                                                                              WO200218632-A2
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide for detecting cytosine methylation SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ33053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; 56pp + Sequence Listing; 56pp; German.
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hes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTTGGCGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.6; DB 6;
Pred. No. 0.47;
22; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic Sample of DNA. The sample is treated chemically to convert CC grosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one member, CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the CC degree of hybridisation to both classes is determined from the label on CC the amplicon. From the ratio of labels hybridised to the two classes of CC oligomers, the degree of methylation is calculated. The method is used: CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs CC and of a wide range of diseases, e.g. cancer, disorders of the central CC nervous, cardiovascular, gastrointestinal and respiratory systems etc., CC particularly by detecting mutations or single nucleotide polymorphisms CC (SNP's); and (ii) for differentiation of cell or tissue types and for crestiques to be determined simultaneously. ABQ13410-CC ABD54121 represent genomic DNA sequences used to illustrate the method CC disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 26
                                                                                                                                                                                               Cytostatic; vaccine; breast cancer marker gene; breast mass; immunos chemotherapy; tumour burden; bait protein; two-hybrid; three-hybrid.
                                                                                                                                                                                                                                                    Breast cancer marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the degree of cytosine diagnosis and prognosis, comprises from chemically treated DNA.
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                                                                                                                                                                                surrogate marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2000; 2000DE-01044543.
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                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                  gene SEQ ID No
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                                                                                                                                                                               pharmacodynamic marker
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19-APR-2002; 2002WO-US012612.

31-OCT-2002. WO200285298-A2

20-APR-2001; 2001US-0285163P

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Best Local Similarity
               WO200168912-A2
                                                                                                    Homo sapiens.
                                                                                                                                                                                               cytosine methylation;
                                                                                                                                                                                                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                           Tumour suppressor gene derived chemically modified sequence #98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS46376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide encoded by breast cancer marker gene, useful for diagnosing, staging, monitoring, prognosing and treating diseases associated with breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 163; 725pp; English
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Pred. No. 0.49,
25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
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RESULT 12
ABL32823
XXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisuphite, of genes associated with tumour suppression and oncogenes CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and CC 500 are missing from the sequence listing) sequences (SS) and sequences (CC oligomer (PNA) of at least 9 nucleic acid may be a peptide nucleic acid complementary to (SS). The nucleic acid may be a peptide nucleic acid conjugate of a set of CC probes for detecting the cytosine methylation state and/or single CC diseases associated with CpG dinucleotides and may form part of a set of CC probes can also be used in a marray for analysing CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The CC potentic parameters for the diagnosis and/or therapy of existing CC diseases or the predisposition to specific diseases, by analysing CC cytosine methylations. The parameters may be compared to another set of CC genetic and/or epigenetic parameters, the differences serving as basis CC patients. The present sequence is one of the 533 genomic sequence of considering odd numbers are the complementary sequence with even corresponding odd numbers are the complementary sequence of the corresponding odd numbers are the complementary sequence of the sequence data for this patent did not form part of the printed corresponding odd numbered sequence (e.g. ID 2 and ID). ID 536 and ID CC sequence data for this patent did not form part of the printed cat form with only might and part of the printed corresponding odd numbers are the complementary sequence of the specification, but was obtained in electronic format directly from WIPO cat first value.
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                         26-MAR-2002
                                                                                                    ABL32823;
                                                                                                                                          ABL32823 standard; DNA; 5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5278 BP; 1569 A; 84 C; 1106 G; 2519 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2000; 2000DE-01013847

06-APR-2000; 2000DE-01019058

07-APR-2000; 2000DE-01019173

30-JUN-2000; 2000DE-01032529

01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 98; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2001; 2001WO-EP002955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-2001.
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                                                                                                                                                                                                                                                 5230
                                                                                                                                                                                                                                                                                                                                5170
                                                                                                                                                                                                                                                                                    66 AAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPIGENOMICS AG
                                                                                                                                                                                                                                             TATGTTTTGGGTAGATATTTATATTATTTTTTAG
                                                                                                                                                                                                                                                                                                                         TATGTAATATTTTTTCGTAGGAGAAATTAGAGGTAAAAGATATATGTTTTTTATTTTT
                                                                                                                                                                                                                                                                                                                                                                   UAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                             16.7%;
ilarity 26.3%;
Conservative 30
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ó
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                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 4; Length 5278; Pred. No. 7.8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                               5264
                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Human immune

system associated

gene

SEQ ID NO:

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RESULT 13
AAZO8975
ID AAZO8
XX AAZO8
XX AAZO8
XX AAZO8
XX 21-OC
XX Straw
XX Recep
KW disea
XX Recep
KW disea
XX Fraga
XX Fraga
XX Fraga
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                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                  21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5278 BP; 1569 A; 84 C; 1106 G; 2519 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 796; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                       Strawberry plant RJ39 promoter DNA
                                                                                                                                                                                     AAZ08975 standard; DNA; 874 BP
  promoter
                                         Fragaria
                                                                 disease
                                                                              Receptacle tissue; tissue-specific expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                        5170
                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                 6 ИАИGИGAИСИИССИЛИССИААЛААЛИСИСИАСАИААЛАСИССАЛЛАСИАИИССИЛИАСИИ 65
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                 resistance;
                                                                                                                                                                                                                                                                              AAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAG 100
                                                                                                                                                                                                                                                                                                        TATGTAATATTTTTTTCGTAGGAGAAATTAGAGGTAAAAGATATATGTTTTTTTATTTTT 522
                                         чевса
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                     TATGTTTTGGGTAGATATTTTATATTATTTTTAG
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000DE-01032529.
2000DE-01043826.
Location/Qualifiers
1. .871
                                                                 insect
                                                                                                                                                                                                                                                                                                                                                                        16.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
                                                                                                                                                                                                                                                                                                                                                           30;
                                                                 resistance;
                                                                                                                                                                                                                                                                                                                                                                        Score 31;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                   ression; transgenic fruit modification;
                                                                                                                                                                                                                                                                                                                                                                        DB 6;
7.8;
                                                                                                                                                                                                                                                     5264
                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                   Length 5278
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                               plant;
                                                                 promoter.
                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 14
ACN44728
ID ACN4
XX
AC ACN4
XX
AC ACN4
XX
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                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the promoter from the RJ39 gene of strawberry CC plants. RJ39 mRNA is expressed in receptacle tissue and expression levels coding sequence was obtained by PCR amplification of strawberry genomic CDNA. A 400 base radiolabelled probe was prepared from the clone and used CC DNA. A 400 base radiolabelled probe was prepared from the clone and used CC containing the promoter and the complete coding sequence. To remove the CC portion of coding sequence, a BglII restriction site was introduced CC upstream of the RJ39 initiation codon by PCR amplification of the CC promoter clone with primers pRJ39-3N1 and T7 promoter primer. Restriction CC digestion produced a truncated RJ39 promoter able to be inserted into a CC digestion produced a truncated RJ39 promoter gene and a termination region cito this vector, a DNA construct can be generated. Once this construct is introduced into a plant, the target gene is expressed in increasing CC levels in receptacle tissue as the fruit matures. Using DNA constructs containing this promoter, it is possible to introduce fruit-specific improvements in plants where the edible fruit comprises receptacle tissue c., strawberries, apples and pears. Such commercially and cresistance to graculturally beneficial modifications may include an increase in the congriser content in fruits, resistance to plant diseases and resistance to
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 2; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9940211-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 874 BP; 265 A; 142 C; 146 G; 321 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA construct for modifying fruit bearing plant phenotype for disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-494302/41.
                                                                                                                                                                                                                                                                                                         597
                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                           UAAGGUUGCGCUUGCCAAUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAG 124
                                                                                                                                                                                             AUCCAGGGACUGUACAGAAUUUUCCUAUACCUCGAGU 161
                                                                                                                                                                                                                                                                                                         ĊĠĀŢĠĊAŢŢĊŢŢĠŢĊĠŦĊĊAĠĀŢŢĂĀĊŢĀŢŢŢĀĀĊĀĀĀŢĀŢĊŢĀŢĀŢĠŢŢ
                                                                                                                                                                                                                                 TATAAATTATATTTATTTTCTAAATTTÄCTTCCATGTTTTTAATTTGCCÄGGTCÄTCGÄT
                                                                                                                                                                                                                                                                                                                                       CUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGU 64
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to increase sugar content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00020033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US002958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Full-length
872. .874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "ATG translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                                                                                                                             16.5%;
                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                            Score 30.6; D
Pred. No. 5.3;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter for RJ39
                                                                                                                                                                                                                                                                                                                                                                                                               BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             start
                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                              Length 874;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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18-NOV-2004

(first entry)

ACN44728;

ACN44728 standard; DNA; 38977

ВP

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ARESULT 15
ADK53988/c
ID ADK539
XX ADK539
XX O6-MAY
DT 06-MAY
DX Plant
XX Plant
XX altere
KW alcoho
KW alcoho
KW branch
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel DNA and protein sequences which Care associated with carcinomas. The sequences are useful for: (i) for Screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (vi) for diagnosing carcinoma; (vii) for neutralizing the effect of AP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma are supplied (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
       altered metabolic characteristic; plant; acid metabolism;
alcohol metabolism; fatty acid metabolism;
branched fatty acid metabolism; alkaloid metabolism;
                                                                            Plant DNA sequence which confers altered metabolic characteristic
                                                                                                                                                     ADK53988;
                                                                                                                                                                                      ADK53988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38977 BP; 10059 A; 9764 C; 9757 G; 9356 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003073826-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytostatic; carcinoma; lymphoma; cancer; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                            30271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                              6 UAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                        CTTATTTTGGTTTCATTTTTAATGCATTTTGTCAGTTTTCTTCATTTTAAAGTCACAAAC 30270
                                                                                                                                                                                                                                                                                                                                                                          AAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGA 125
                                                                                                                                                                                                                                                                                                       uccaeggacuguacagaauuuuccuauac 154
                                                                                                                                                                                                                                                                                                                                                                                                               TCTTTGCTGCTTTTTTAATCTTTAAATTTTCTTACAAAAATTTCAATTTTTGTTGATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO 1321; Opp; English.
                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%;
                                                                                                                                                                                    667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mCG2727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30.6; DB 11;
Pred. No. 24;
5; Mismatches 74;
                                                                                                                                                                                                                                                                        30299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 38977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Search completed: December 22, Job time: 271.794 secs

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Matches 45
                                                                                                                                                                                                                                                                                                               The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered amino acid metabolism, altered ester metabolism, altered glyceride metabolism, altered phenolic metabolism, altered carbohydrate metabolism, altered skyrom entabolism, hydrocarbon metabolism, altered or akynom entabolism, hydrocarbon metabolism, ketone or altered siease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid metabolism; ester metabolism; glyceride metabolism; phenolic metabolism; carbohydrate metabolism; sterol metabolism; terpene metabolism; isoprenoid metabolism; alkene metabolism; alkyne metabolism; hydrocarbon metabolism; ketone metabolism; alkyne metabolism; disease resistance; gene shuffling; sexual PCR; quinone metabolism; disease resistance;
                                                                                                                                                                                                                                                                  Sequence 667 BP; 220 A; 141 C; 117 G; 189 T; 0 U; 0 Other;
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AGROSCIENCES LLC.
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| 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.2 | 32.4 | 32.4 | 32.4 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.8 |
| 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.2 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 | 17.4 | 17.4 | 17.4 | 17.5 | 17.5 | 17.5 | 17.5 | 17.5 | 17.5 | 17.6 |
| 886 | 880 | 770 | 739 | 706 | 609 | 533 | 1018 | 890 | 822 | 704 | 388 | 284 | 1321 | 873 | 560 | 981 | 735 | 717 | 635 | 594 | 424 | 932 |
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| CC338258 | BU718281 | CC621028 | BZ993539 | CC340483 | BH641477 | BH641302 | AG374941 | CC080461 | CV674373 | BZ088228 | B90539 | AA331426 | CC281519 | BH092133 | BX197395 | CC003308 | CV523850 | CW016619 | CV658370 | CE633830 | CD473048 | CG419370 |
| CC338258 OGUCA27TH | BU718281 SJM2CHF04 | CC621028 OGKAB07TV | BZ993539 PUFIO35TB | CC340483 OGTAE45TV | BH641477 1008048A0 | BH641302 1008046F0 | AG374941 Mus muscu | CC080461 CSU-K33r. | | BZ088228 lkx77a07. | B90539 CIT-HSP-217 | AA331426 EST35414 | CC281519 CH261-25E | BH092133 RPCI-24-3 | BX197395 Danio rer | CC003308 PUDEK75TD | CV523850 Mdlv2_401 | CW016619 ZMMBLc000 | CV658370 Mdlv2_402 | CE633830 tigr-gss- | CD473048 nad03-11m | CG419370 ZMMBBC002 |

TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CO153155 LOCUS 밁 REFERENCE AUTHORS ð ORIGIN FEATURES DEFINITION Query Match Best Local Similarity Matches 51; Conserv source 88 Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: EN.14 row: A column: 1 High quality sequence stop: 383. Drosophila melanogaster (fruit fly) Drosophila melanogaster Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 433) CO153155 433 bp mRNA linear EST 05 EN01401.5prime Exclixis FlyTag MN08 BlueScript Drosophila melanogaster cDNA clone EN01401 5, mRNA sequence. CO153155 CO153155.1 GI:48907156 Exelixis FlyTag EST Project MN08 Library Unpublished (2004) Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Platt, D. and Swimmer, C. TSE Contact: Stapleton, M. Conservative /clone lib="Exelixis FlyTag MN08 BlueScript" /note="Vector: pBluescript; Site 1: NotI; Site_2: oligodT primed from LPS induced mbn2 cell line." /organism="Drosophila melanogaster" /mol type="mRNA" /db_xref="taxon:7227" /clone="EN01401" Location/Qualifiers 19.6%; Score 36.4; DI 38.6%; Pred. No. 1.4; tive 28; Mismatches DB 7; Length 433; Insecta; Pterygota; era; Muscomorpha; Indels EST 05-OCT-2004

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         CO153765 490 bp mRNA linear EST 0: EN02756.5prime Exelixis FlyTag MN08 BlueScript Drosophila melanogaster cDNA clone EN02756 5, mRNA sequence. CO153765 CO153765 GI:48907766 EST.
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Plate: EN.20 row: A column: 10
High quality sequence stop: 412.
Location/Qualifiers
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Drosophila melanogaster
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One Cyclotron Rd, Berkeley, CA
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/note="Vector: pBluescript; Site_1: NotI; Site_2: XhoI;
oligodT primed from LPS induced mbn2 cell line."
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/mal_type="mRNA"
/db xrefe="taxon:7227"
/clone="EN02010"
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                  Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
Plate: EN.153 row: B column: !
High quality sequence stop: 474
                Email: http://www.fruitfly.org/EST, Plate: EN 153 row: B column: 5
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Nakanishi,M., Muzong,C., Peterson,E., Laufer,A.,
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Bukaryota, Metazoa, Arthropoda; Brachycera; Muscomorpha;
Rephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 490)
1 (Dases 1 to 490)
1 Nakanishi, M., Muzong, C., Peterson, E., Laufer, A., Leung, W., Platt, D.
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Fax: 510 486 6798
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Plate: EN.27 row: E column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720,
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Location/Qualifiers
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/note="Vector: pBluescript; Site_1: NotI; Site_
oligodT primed from LPS induced mbn2 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Drosophila melanogaster"
|mol_type="mRNA"
|db_xref="taxon:7227"
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                                                                     94720, USA
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                                  est@fruitfly.berkeley.edu
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                                                                                                                                                                                       Leung, W., Platt, D.
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Gaps

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 723)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG777039 723 bp n
602664245F1 NIH_MGC_59 Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG777039.1 GI:14047356
EST.
                                                                                                                                                                                                                                                                 High quality sequence stop: 688.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAATATCCAGG 216
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                                                                                                                                                                                                                                                                                                         LLCM1664 row: i column: 11
         /tissue_type="mucoepidermoid carcinoma"
/lab_host="NHIOS (T] phage-resistant)"
/clone_lib="NIH_MGC_59"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (ggccattatggcc);
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACCGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCCGGCCGACATG-dT(30)BN-3'
sequence: 5'-ATTCTAGAGGCCGAGCCGGCCGACATG-dT(30)BN-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site 1: NotI; Si
oligodT primed from LPS induced mbn2 cell li
                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4809682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
|mol_type="maNA"
|db_xref="beaxon:7227"
|clone="EN15317"
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Pred. No. 1.
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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664 CCTGACCAG 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         544 TCTTGCTCTGGAACAACACTTTCCCTGCTCATTGAGAGGATTGCGAATGCTTAGGTTC
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BB446527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kiyosawa, H., Kojima, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, A., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Shibata, K., Yamanaya, T., Tsunoda, Y., Watahiki, A., Yoshida, K., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Yawashiri, Y., Soshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), $20-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai, Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Okazaki,Y. and Hayashizaki,Y.
Okazaki,Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermoactivation of thermolabile enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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316 bp mRNA linear EST 19-JUL-2
BB446527 RIKEN full-length enriched, 9 days embryo Mus musculus
CDNA clone D030056G07 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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Pred. No. 6;
21; Mismatches
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                                                                                                                                                                                                  Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                      Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                         Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Characteristics of the Lotus japonicus gene repertoire deduced large-scale expressed sequence tag (EST) analysis plant Mol. Biol. 54 (3), 405-414 (2004)
                                                                                                                                                                                                                                                                                        EST
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BP040755 Lotus corniculatus var. japonicus flower bud Lotus corniculatus var. japonicus flower bud Lotus corniculatus var. japonicus cDNA clone MFB093a04_f 3', mRNA
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                                                                                                                                                                           (bases 1 to 616)
1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.l
Location/Qualifiers
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/clone="D030056G07"
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lab_host="DH10B"
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Pred. No. 5.8;
          URL:http://www.kazusa.or.jp/en/plant/.
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                                                             342 TGACTGTGAGGCCTTGGTTTGTAAGGATTCTCTGAGCCCCAGTTTGTCATGTGTTGCTAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 UCCAACAAGAUCCAGGGACUGUACAGAAUUUUUCCUAUACCUCGAGUCGGGUUUGGA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 TGCTATCGAGAAGCTTTTGATGTTTTTATTGTATATAACGGACTTTGTAAGGAAGCAC 515
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                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I (bases 1 to 651)
Kirkness, E.F., Bafna, V., Halpern, A.L., Rusch, D.B., Delcher, A.L., Pop, M., Wang, Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tigr-gss-dog-17000360210705 Dog genomic survey sequence. CE302369
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                   Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (dog)
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                             agunaageungcecuneccuaunnagecanacunc 96
                                                                                           UGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAU 61
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                                                                                                                                                                                                                                                                                                                                                  shotgun
                                                                                                                                                                                                     /organism="Canis familiaris"
/mol_type="genomic DNA,"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="851te 1: BatXI; Libraries we peripheral blood"
                                                                                                                                                                                                                                                                                                                                                               ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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/clone="MFB093004_f"
/tissue_type="flower bud"
/clone_Tib="Lotus_corniculatus_var._japonicus_flower_bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lotus corniculatus
/mol_type="mRNA"
/isolate="Miyakojima_MG-20"
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                                                                                                                                           18.4%;
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24; Mismatches
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23; Mismatches
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clone cr2-00032-h1 5', mRNA sequenc
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Gp mxAB 01811 M13R mxA Gammarus mxNA sequence.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gammarus pulex
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Peracarida; Amphipoda; Gammaridea; Gammaroidea;
                                                                   CB797617
CB797617.1 GI:29886094
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRIMETS
FORWARD: M13F (GGTTTCCCAGTCACGACGTT)
FORWARD: M13F (CAGGAAACAGCTATGACCATG)
BACKWARD: M13F (CAGGAAACAGCTATGACCATG)
Seq primer: M13F (CAGGAAACAGCTATGACCATG)
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BIOSI 1, School of Biosciences,
Cardiff, CF10 3TL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammarus pulex response to oestrogen and testosterone (2005)
Unpublished (2005)
Contact: Christine Sambles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaridae; Gammarus.

1 (bases 1 to 544)
Sambles, C., Richards, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: gamblescm@cardiff.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                  AAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGUUAAGGUUGCGCUUGCCCUAUUUAG 87
                                                                                                                                                                                                                                        CATATACCAC 313
                                                                                                                                                                                                                                                                                                          GAATATAACCGAAGATCTTCAATCAGTGTTCGACTAGATACATTAACTATATACATTTTC 323
                                                                                                                                                                                                                                                                                                                                           GCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGAUCCAGGGACUGUACAGAAUUUU 147
                                                                                                                                                                                                                                                                          CCUAUACCUC 157
                                                                                                                                                                                                                                                                                                                                                                             AACAATTGCATATGAAAGACGAATTGGTACGTATATTTGATCTAGATGCGTCCTGTCACG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 448.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:52641"
/clone="Gp_mxAB_01B11"
/sex="Mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="mxA"
/note="Vector: pBluescript II SK+; Site_1: XhoI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Gammarus pulex"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardiff University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA linear EST 11-MAY-2005 pulex cDNA clone Gp_mxAB_01B11 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 544;
                                                                                                                                      (10398)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                         Rattue
                                                                                                                                      norvegicus cDNA
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AUTHORS
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CW305721/c
LOCUS
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AUTHORS
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Best Local
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                                                         source
                                                                                                            Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 791 row: d column: 03
Seq primer: Swfor Forward
Class: methylation filtered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 TTGTTAATTCTAACTTTTATTCCTTATACAATTTGCAGAATAGAGTTGAAATGATTGCTG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 UAGUUAAGGUUG 72
                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 639)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
Martienssen,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CW305721 639 bp DNA linear GSS 31-OCT-2004 104 791_11466459_148_36273_014 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11466459, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 UUGACUAUGUGAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUA 60
                                                                                                                                                                                                                                 Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 421)
Amgen EST Program.
Amgen Rat EST Program
                                                                                                                                                                                                                                                                                                             Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CW305721.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciurognathi; Muroidea; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                        Contact: Bedell JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amgen, Inc
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                                                                         quality sequence stop: 639
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              032 row: h column:
Location/Qualifiers
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/clone_Tib="Colon Rat 2 (10398)",
/note="Vector: pMoB; Site 1: null;
/ Fetal rat intestinal library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="cr2-00032-h1"
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38.9%; Pred. No. 11;
tive 20; Mismatches
                                                                                                                                                                                                                                   St.
                                                                                                                                                                                                                                   Louis,
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             Matches
                                                                                      Query Match
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                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 ACCUCGAGUCGGGGUUGGAAUCUAAGGU 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unite de Recherche des Produits de la Vigne Institut National de la Recherche Agronomique 2, place Viala, 34 060 Montpellier Cedex 01, I Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitise.

1 (hases 1 to 1334)
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EST 935 Green Grape berries Lambda Zap II Library Vitis vinifera
CDNA Clone GB009A01 3', mRNA sequence.
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Unpublished (2002)
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BQ798766.1 GI:22013732
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             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        romieu@ensam.inra.fr
                                                                                                                                                                                                   /dev_stage="green stage"
/clone lib="Green Grape berries Lambda Zap II Library"
/note="Gran: Fruit; Vector: Lambda Zap II; Site_1: Eco
RI; Site_2: XhoI; Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seds) at various developmental stages by Terrier,N.,
Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158
(12): 1575-83 2001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:29760"
/clone="GB009A01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cultivar="Shiraz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Vitis vinifera"
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104)"
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/clone="11466459"
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                                           18.1%;
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50.0%; Pred. No. 12;
tive 10; Mismatches
                                           Score 33.6;
Pred. No. 19
Mismatches
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    29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genom Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                       further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACATCATTAAATATGTATCTCACAGTTGAAAAGATTAGTATACTTAGAGTTTCACACCT 231
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/clone_lib="RIKEN full-length
                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A430045020"
                                                        tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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                                                                                                                                                                                                                                                                                                       cells of the sea urchin embryo Development 128 (13), 2615-2627
                                                                                                       NCBI Trace Archive: 490865972
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                                                                                                                                                                              Fax: 713-798-6977
                                                                                                                                                                                                                One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                               Human Genome Sequencing Center
Baylor College of Medicine
                                                                                                                                                                                                                                                                     Contact: Erica Sodergren
                                                                                                                                                                                                                                                                                                                                                           Ettensohn, C.A.
                                                                                                                                                                                                                                                                                                                                                                              Zhu, X., Mahairae, G., Illiee, M.R., Cameron, R.A., Davidson, E.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus
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                                                                                                                                                                                                                                                                                                                                            large-scale analysis of mRNAs expressed by primary mesenchyme
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/mol type="mRNA"
/db_xref="taxon:7668"
/clone="PMCSPR2-127020"
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                                                                                        Location/Qualifiers
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QBH11h11.pg (
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                                                                                                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante.info.infobiogen.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF002460.1
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Unpublished (2003)
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dt priming from poly A+ RNA, directionally cloned"
                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/clone="QBH11h11"
                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea Urchin primary mesenchyme cell
                                                                                                                                                                                                                                                                  /tissue_type="sheath (in)"
/clone_lib="QBH"
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="embryo"
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Best Local S
Matches 51
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Patent No. 6703491
GENERAL INFORMATION:
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| 27.2 27.2 | 27.2 | 27.2 | 27.2 | 27.2 | 27.2 | 27.4 | 27.6 | 27.6 | 27.6 | 27.6 | 27.6 | 27.6 | 27.6 | 27.6 | 27.6 | 27.8 | | 27.8 | 27.8 |
| 14.6 | 14.6 | 14.6 | 14.6 | 14.6 | 14.6 | 14. | 14.6 | 14.8 | 14.8 | 14.8 | 14.8 | 14.8 | | 14.8 | 14.8 | 14.9 | 14.9 | 14.9 | 14.9 |
| 1179 | 601 | 601 | 601 | 601 | 568 | 7 83516 | 109378 | 3 107941 | 3 41684 | 3 41594 | 18554 | 18554 | 4080 | 3 2669 | | 118382 | 118382 | | 25249 |
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| US-08-336-778-3 US-09-710-279-1199 | US-09-949-016-158966 | US-09-949-016-158965 | US-09-949-016-23558 | US-09-949-016-23557 | US-09-270-767-26859 | US-09-949-016-15378 | US-09-949-016-12391 | US-09-949-016-14206 | US-09-536-059-1 | US-09-949-016-17298 | US-10-652-164-3 | US-09-811-825A-3 | US-09-016-434-1342 | US-09-976-594-679 | US-09-949-016-87413 | US-09-949-016-15997 | US-09-949-016-15996 | US-09-949-016-15825 | US-09-949-016-17444 |
| Sequence 3, Appli Sequence 1199, Ap | Sequence 158966, | Sequence 158965, | Sequence 23558, | Sequence 23557, | Sequence 26859, | Sequence 15378, | Sequence 12391, | Sequence 14206, | Sequence 1, Appli | Sequence 17298, A | Sequence 3, Appli | Sequence 3, Appli | Sequence 1342, A | Sequence 679, Ap | Sequence 87413, A | Sequence 15997, | Sequence 15996, . | Sequence 15825, A | Sequence 17444, A |

ALIGNMENTS

Drosophila melanogaster

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Sequence 16354, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 199-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                RESULT 2
US-09-270-767-16354
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; ORGANISM: Drosophila melanogaster
US-09-270-767-1072
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1072

LENGTH: 1345
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                                                                                                                      Drosophila melanogaster
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US-09-949-016-17150
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Sequence 17150, Application US/09949016
Patent NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09020033A
Patent No. 6043410
GENERAL INFORMATION:
APPLICANT: Wilkinson, Jack Q.
TITLE OF INVENTION: Strawberry Fruit Promoters for Gene Expression
FILE REFERENCE: Strawberry Promoters for Gene Expression
CURRENT APPLICATION NUMBER: US/09/020,033A
CURRENT FILING DATE: 1998-02-06
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
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LENGTH: 1345
TYPE: DNA
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NAME/KEY: promoter
LOCATION: (1)..(874)
OTHER INFORMATION: RJ39C promoter
-09-020-033-2
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TYPE: DNA
ORGANISM: Fragaria vesca
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Local Similarity 38.6%;
les 51; Conservative 28
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                                                                                                                                                                                                                                     CTAATTACACGGTAGAGAATACTCATGAAACTGGAAT 753
                                                                                                                                                                                                                                                                          AUCCAGGGACUGUACAGAAUUUUÇCUAUACCUCGAGU 161
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28.7%; Pred. No. 2.8;
ative 33; Mismatches
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Patent No. 6028250
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  APPLICATION NUMBER: PCT/JP96/00777
FILING DATE: 26-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 30-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT:
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ADDRESSEE: BROWDY AN
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APPLICANT: KATO, İKUNOSHİN
TITLE OF İNVENTION: PLANT PROMOTER AND METHOD FOR GENE
TITLE OF İNVENTION: EXPRESSION USING SAID PROMOTER
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                                                                  NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
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l Similarity 26.4%;
38; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANMA, Yoshiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BROWDY AND NEIMARK, P.L.L.C. 9 7th Street N.W., Ste. 300
   (202)
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Pred. No. 1
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Patent No. 6924097
GENERAL INFORMATION:
APPLICANT: OHBA, Toshiharu
TAKNHASHI, Shuichi
                                                                                                                           NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: OHBA-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 29.7 Matches 27; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 2960 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                               PRIOR APPLICATION: «Unknown»

APPLICATION DATA:
APPLICATION NUMBER: US/08/913,842
PILING DATE: 30-Sept-1997
APPLICATION NUMBER: JP 07-073043
PILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/JP96/00777
PILING DATE: 26-MAR-1996
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 7th Street N.W., Ste. 300
TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 ATTGCCTCTTTTACATGTTTTTATATAG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CUUGCCUAUUUAGGCAUACUUCUCAGGAUGG 105
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                                                          LENGTH: 2960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/368,572 FILING DATE: 05-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANMA, YOShiko
ASADA, Kiyozo
KATO, Ikunoshin
INVENTION: PLANT PROMOTER AND METHOD FOR GENE
EXPRESSION USING SAID PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                         OHBA=1
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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-455-550-7
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Patent No. 5670338
   Matches
                Query Match
Best Local S
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                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
TELEX: 200291
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/056,51
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,81
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Eisenstein, Ronald I
                                                                                                                     MOLECULE TYPE: cl
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0:
FILING DATE: 31-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MURAKAMI, KI
APPLICANT: UENO, NAOTO
APPLICANT: KATO, YUKIO
                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                          STRANDEDNESS:
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2h 15.9%; Score 29.6; DB 2; Length 19
| Similarity 42.6%; Pred. No. 7.3;
| Conservative 15; Mismatches 24; Indels
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MA
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                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 30.2; DB 3; 29.7%; Pred. No. 5.7;
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                                                                                                                                                                                                                                                                                                                                                                  30628
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                                    Length 1558;
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US-09-949-016-16994
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; LOCATION: (1)...(46718)
; OTHER INFORMATION: n = A,T,C
US-09-816-093-3
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US-09-816-093-3
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                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                               NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16994
LENGTH: 36755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16994, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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APPLICANT: GAN, Weiniu et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09816093 Patent No. 6518055
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                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 46718
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/816,093
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001182
                                                     ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 15.9%;
Local Similarity 32.6%;
nes 43; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10211 TTTGAATGGAAT 10222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10151 GGGCTTTTGTTTATGGCTGCTTAGGGGCTTAAAAGCTCCATGGACTGGTGAGGATTATCA 10210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 UUAAGGUU 71
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                                                                                                                                                                                       2000-09-08
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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Query Match
Best Local Similarity
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/211,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08
; ORGANISM: Human US-09-949-016-170384
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                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 170384
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Patent No. 6610906
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 170384, A
Patent No. 6812339
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
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Best Local
                                                                                                                                   NUMBER OF SEQ ID NOS:
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CURRENT APPLICATION NUMBER: US/09/328,925
CURRENT FILING DATE: 1999-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kurachi, Kotoku
APPLICANT: Kurachi, Sumiko
TITLE OF INVENTION: Nucleotide Sequences for
TITLE OF INVENTION: Use Thereof
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ORGANISM: Homo sapiens
                                                                   LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9983 TGCAAAGACCTATTTGGACTAACTT 9959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GAUCUUGCUUUCGUAAUAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGUUAAGGU 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
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OF DETECTION AND USES THEREOF
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15.4%; 35.7%;

Score Pred.

28.6; No. 12;

DΒ

3

Length 601;

LENGTH: 102520

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-33
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241.755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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LENGTH: 94142
                                                                                                                                                                                                                                                                                                                                                                    Sequence 17367, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity
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NUMBER OF SEQ I
SOFTWARE: FABLS
SEQ ID NO 17367
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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LOCATION: (1)...(94142)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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                    SEQ ID NOS: 207012
FastSEQ for Windows Version
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35.7%; Pred. No. 58;
rative 20; Mismatches
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OF DETECTION AND USES THEREOF
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OF DETECTION AND USES THEREOF
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RESULT 15
US-09-949-016-105589
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US-09-949-016-17367
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                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                          Sequence 105589, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12448
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            CURRENT FILING DATE: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CL001307
CURPERNY PORTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
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ORGANISM: Human
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FILING DATE: 2000-09-08
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41.2%; Pred. No. 80;
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Pred. No. 80;
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                               Score
seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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US-10-363-345A-19643
US-10-363-345A-19644
US-10-363-483A-19644
US-10-363-483A-19644
US-10-363-483A-19644
US-10-363-483A-19644
US-10-363-483A-19644
US-10-972-079-54259
US-10-925-065A-706872
US-10-027-632-174581
US-10-027-632-174581
US-10-11-455-796
US-10-027-632-245598
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US-10-088-750B-3
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Sequence 4, Appli
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Sequence 19643, A
Sequence 19644, A
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             245597,
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9972, Ap
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| 29.6 | 29.6 | 29.6 | 29.8 | 29.8 | 29.8 | 29.8 | 29.8 | 30 | 30 | 30 | 30.2 | 30.2 | 30.2 | 30.4 | 30.4 | 30.4 | 30.4 | 30.6 | 30.6 | 30.6 | 0.0 |
| 15.9 | 15.9 | 15.9 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.1 | 16.1 | 16.1 | 16.2 | 16.2 | 16.2 | 16.3 | 16.3 | 16.3 | 16.3 | 16.5 | 16.5 | 16.5 | 10.0 |
| 199 | 180 | 180 | 2140405 | 2140405 | 44752 | 1296 | 600 | 495 | 492 | 478 | 706 | 640 | 201 | 96589 | 776 | 776 | 667 | 38977 | 38090 | 4236 | 1760567 |
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| US-10-088-750B-2 | US-10-085-783A-40622 | US-10-242-535A-40622 | US-10-027-632-76212 | US-10-027-632-76212 | US-10-741-600-17553 | US-09-974-300-2665 | US-10-972-079-39850 | US-09-925-065A-304014 | US-10-357-930-46627 | US-09-864-761-11439 | US-10-424-599-83152 | US-09-925-065A-795140 | US-10-741-600-18334 | US-10-085-117-130 | US-09-925-065A-670469 | US-09-925-065A-670468 | US-10-487-901-1371 | US-10-087-192-1321 | US-10-085-117-211 | US-10-085-117-212 | 00-TO-001-000-T-400 |
| Sequence 2, Appli | Sequence 40622, A | Sequence 40622, A | Sequence 76212, A | Sequence 76212, A | Sequence 17553, A | Sequence 2665, Ap | Sequence 39850, A | Sequence 304014, | Sequence 46627, A | Sequence 11439, A | Sequence 83152, A | Sequence 795140, | Sequence 18334, A | Sequence 130, App | Sequence 670469, | Sequence 670468, | Sequence 1371, Ap | Sequence 1321, Ap | Sequence 211, App | Sequence 212, App | peducire Title |

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                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 5
LENGTH: 198
TYPE: RNA
ORGANISM: Triatoma Virus
                                                                                                                                                                                                                                                                                                                  Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKASHIVA, Nobuhiko
APPLICANT: NAKASHIVA, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: A ctivity
FILE REFERENCE: 3190-015
FURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT APPLICATION NUMBER: JP 2001-016746
PRIOR APPLICATION NUMBER: JP 2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
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181
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                                                                                                                                                                                                                                                                                                                                  h 100.0%; Score 186; DB 7; Length 198; Similarity 100.0%; Pred. No. 3e-51;
                                                                                               CAAGAUCCAGGGACUGUACAGAAUUUUCCUAUACCUCGAGUCGGGUUUGGAAUCUAAGGU 180
                                     UGACUC
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UGACUC 186
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                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10088750B
Publication No. US20040166486A1
GEMERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: ACCIVITY
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT APPLICATION NUMBER: US/0641
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-31
NUMBER: PCT/JP01/00641
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APPLICANT: NAKASHMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SDETWARE: Patentin version 3.2
SEQ ID NO 3
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
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                                                                                                                                                                                                                             LENGTH: 200
TYPE: RNA
ORGANISM: Cricket Paralysis Virus
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TYPE: RNA
ORGANISM: Drosophila C Virus
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                                                                              70 UUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAAGAACAAGAUCCA 129
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                                                                                                                              l Similarity
45; Conserv
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79; Conserv
                                            UUUAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCA 130
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                                                                                                                                Conservative
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                                                                                                                                               18.1%;
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                                                                                                                            Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                 Score 33.6;
Pred. No. 1.
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                                                                                                                                                              DB 7;
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                                                                                                                                                                Length 200;
                                                                                                                            Indels
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US-10-363-345A-19644/c
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US-10-363-345A-19643
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US-10-363-345A-19643
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CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 19644
LENGTH: 854
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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SEQ ID NO 19643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE: E01/1227
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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ORGANISM: Artificial Sequence
FEATURE:
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73 CGCUUGCCUAUU
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Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
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CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 19643
LENGTH: 854
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Best Local (
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Publication No. US20050064401A1
                                                                                                                                                                Matches
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Best Local !
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 19644
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic
OTHER INFORMATION: CPG-island No: 19643
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                                                                                                                                                                                    Local
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Local Similarity 36.1%;
Les 26; Conservative 2
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                                                                              274 TGTTTTTTTGGTTAAAAGATTTGGATATAAAAGTCGTGAGTTTTTTATGGTTGGGGTCG 215
214 GGGTTGGCGAGT 203
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                                    CGCUUGCCUAUU 84
                                                                                                                                                                  Conservative
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Pred. No. 2.3;
                                                                                                                                                              Mismatches
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US-10-125-968-540
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           TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF TITLE OF INVENTION: LIVESTOCK FILE REFERENCE: MMI1110-2 CURRENT APPLICATION NUMBER: US/10/972,079 CURRENT FILING DATE: 2004-10-22 PRIOR APPLICATION NUMBER: US 60/514,333 PRIOR FILING DATE: 2003-10-24 NUMBER OF SEQ ID NOS: 96631 SOFTWARE: PatentIN version 3.1

SEQ ID NO 54259

LENGTH: 600
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APPLICANT:
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CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,163
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 1417
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 315, 323, 352, 411
OTHER INFORMATION: n = A,T,C or G
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 17.8%; Local Similarity 34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 AAACACTTTTCGGCCCGCTCTTAGAAACTA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 TAAGGGTTTCACATTAAATTTAAACATACTTATATTTTATAACCAAACAAGTCATATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 GGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGAUCCAGGGACUGUACAGAAUUU 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 UAAAAUCUGUACAUAAAAGUCGAAAGUAUUGCUAUAGGUUAAGGUUGCGCUUGCCUAUUUA 86
                                                                                                                                                                                                                                                DeNISE, Sue K.
ROSENFELD, David
KERR, Richard
BATES, Stephen
HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UCCUAUACCUCGAGUCGGGUUUGGAAUCUA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCATACTCATTAGGATTGAGTGCTTTCTTACACCCAAAATACATGTATACAAAAGATTTA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palermo, Adam
Wang, Youzhen
Steinmann, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elias, Josh
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; Pred. No. 2.3;
25; Mismatches
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREESEQ FOR WINDOWS Version 4.0
SEQ ID NO 706871
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-706871
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                                                                                                                   RESULT 11
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US-09-925-065A-706871/c
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US-10-972-079-54259
Sequence 706872, Application US/09925065A Publication No. US20050228172A9
GENERAL INFORMATION: APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 706871, Application US/09925065A Publication No. US20050228172A9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                 y Match 17.3%; Score 32.2; Di Local Similarity 34.0%; Pred. No. 7.8;
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                                                                                                                                                                      575
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                                                                                                                                                                                                                                                                                                         TTÄTTÄTÄACATTÄATTÄGÄÄAGGGCÄTGCÄTTGCCÄTCCTTGGAATTTCCTTCGCATTT 636
                                                                                                                                                                                                     UUUUCCUAUACCUCGAGUCGG 164
                                                                                                                                                                                                                               UUAGGCAUACUUCUCAGGAUGGCGGUUGCAGUCCAACAAGAUCCAGGGACUGUACAGAA 143
                                                                                                                                                                      TGGTAAGTTAAGTGGAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UAGUUAAGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAA 120
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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   of Single
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FILL REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT ELLING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-05-09
NUMBER OF SEG ID NOS: 957086
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 706872
                                                                                                                                                                                                                                                                                US-10-425-115-9972
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; ORGANISM: Homo sapiens
US-09-925-065A-706872
                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 9972
LENGTH: 2908
TYPE: DNA
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                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE DEPERANCE CAO.
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Best Local
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                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: MRT4577_109093C.1
                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
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                                                                                                                                                                                                            Local Similarity
    543
                                           153 ACCUCGAGUCGGGUUUGGAAUCUAAGGU 180
                                                                                              483
                                                                                                                                          93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   575 TGGTAAGTTAAGTGGAGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        635 TAAAATACATTTTTAAGGAGGGAGAGAAGGAGTTGAAAGTGATTTACAAATTAAAAAAA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695 TTATTATAACATTAATTAGAAAGGGCATGCATTGCCATCCTTGGAATTTCCTTCGCATTT 636
                                                                                                                                                                                        44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 ИААИАААНСИСИАСАИААААСИССААААСИАИИССИАИАСИИААССИИСССИИИ
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Similarity 34.0%; Pred. No. 7.8;
48; Conservative 25; Mismatches
CGCGCGAGACCGAGCGGGGGGCGCCAAGGT 570
                                                                                     CTCTCCACGAAGGCGTGCTCCTTCTACAAGATCCACGGGCCCGACCGCATCATCCTAT 542
                                                                                                                              CUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGAUCCAGGGACUGUACAGAAUUUUCCUAU 152
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                       17.2%;
                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                       Score 32; DB 8; Length 2908; Pred. No. 13;
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; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(713059)
; OTHER INFORMATION: n = A
US-10-027-632-174581
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                                                                    FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 174581, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                               APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/193, 483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185, 218 PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513099 AAGTCGTTCTTTCAAAGTTATGTAAATTTTACCTGA 513134
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APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGTCGTTTGCACAACAATGTCTATAAACTTAAGGCAATAGGATTGTTCTCTTAA 513098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGUUGCGCUUGCCUAUUUAGGCAUACUUCUCAGGA 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%; Score 32; DB 5; 37.5%; Pred. No. 1.4e+02;
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Search completed: December 22, 2005, 16:21:18 Job time : 439.953 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 105212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 105212, Application US/10425115 Publication No. US20040214272A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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NAME/KEY: misc_feature
LOCATION: (1)...(713059)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 1038
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                                                                                                                 63 GUUAAGGUUGCGCUUGCCUAUUUA 86
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                                                                                                                                                                                                                                                  16.8%; Score 31.2; 1 38.1%; Pred. No. 15;
                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                    DB 8;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                             is derived by analysis of the total score distribution.
     2222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             December 22, 2005, 08:40:58; Search time 169.584 Seconds (without alignments) 569.190 Million cell updates/sec
                         15.5 1210

15.3 189252

15.2 207835

15.2 207835

14.2 207835

14.8 2613

14.6 2130

14.6 2130

14.6 3153

14.6 4845

14.6 4845

14.6 160170

14.5 102186

14.5 102186

14.5 10221

14.4 16021

14.4 16021
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186
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length DB
US-10-750-185-35479
US-10-750-185-3393
US-10-750-185-3180
US-10-95-561-13259
US-11-121-086-39
US-11-121-086-39
US-11-121-086-39
US-11-121-086-39
US-11-121-086-31
US-10-793-626-3159
US-10-793-626-3350
US-10-623-155-151
US-10-623-155-151
US-10-623-155-335
US-11-121-086-32
US-11-121-086-32
US-11-121-086-32
US-11-121-086-32
US-11-121-086-33
US-11-121-185-2623
US-11-175-185-25738
US-11-750-185-25738
US-10-750-185-25738
US-10-750-185-25738
US-10-750-185-25738
US-10-750-185-25738
US-10-750-185-25738
US-10-750-185-25738
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                                                                             Sequence 55479, A Sequence 43180, A Sequence 43180, A Sequence 13259, A Sequence 13259, A Sequence 39, Appl Sequence 10, Appl Sequence 17, Appl Sequence 1199, Appl Sequence 3411, App Sequence 3411, App Sequence 351, App Sequence 37, Appl Sequence 37, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 190, Appl Sequence 202, Appl Sequence 202, Appl Sequence 202, Appl Sequence 202, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequence 203, Appl Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
     RESULT 2
US-10-750-185-33993/c
Sequence 33993, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 |
| 25.8 | 25.8 | • | 25.8 | 25.8 | 25.8 | 26 | 26 | 26 | 26 | 26.2 | 26.2 | σ | 26.2 | σ | 26.4 | 26.4 | 26.6 | 9 | • | 26.6 | 9 |
| 13.9 | 13.9 | 13.9 | 13.9 | 13.9 | 13.9 | 14.0 | 14.0 | 14.0 | 14.0 | 14.1 | 14.1 | 14.1 | 14.1 | 14.2 | 14.2 | 14.2 | 14.3 | 14.3 | 14.3 | 14.3 | 14.3 |
| 1545 | 1473 | 1467 | 1419 | 1419 | 600 | 2231 | 2076 | 1392 | 1200 | 5873 | 2546 | 1931 | 1162 | 1685 | 1286 | 984 | 319608 | 65723 | 2734 | 2513 | 2010 |
| 9 | თ | σ | 9 | σ | σ | σ | σ | σ | σ | σ | σ | ð | σ | σ | σ | σ | 7 | 9 | σ | 0 | σ |
| US-10-750-185-53618 | US-10-508-263-9 | US-10-508-263-11 | US-10-508-263-63 | US-10-508-263-61 | US-10-750-185-469 | US-10-750-185-53949 | US-10-750-185-61396 | US-10-750-185-31869 | US-10-750-185-38659 | US-10-750-185-45477 | US-10-750-185-31825 | US-10-750-185-64161 | US-10-750-185-61391 | US-10-750-185-59057 | US-10-750-185-62661 | US-10-750-185-29534 | US-11-145-703-1 | US-10-995-561-13200 | US-10-510-386-5 | US-10-750-185-64578 | US-10-750-185-61522 |
| Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| 53618, A | 9, Appli | 11, Appl | 63, Appl | 61, Appl | 'n | 53949, A | 61396, A | 31869, A | 38659, A | 45477, A | 31825, A | 64161, A | 61391, A | • | 62661, A | 29534, A | 1, Appli | 13200, A | 5, Appli | 64578, A | 61522, A |

ALIGNMENTS

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RESULT 1
US-10-750-185-55479
; Sequence 55479, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
   APPLICANT: MMI GENOMICS, INC.
   APPLICANT: MOISE Sue K.
   APPLICANT: MOISE Sue K.
   APPLICANT: ROSENFELD, David
   APPLICANT: HOLM, Tom
   APPLICANT: HOLM, Tom
   APPLICANT: HOLM, Tom
   APPLICANT: PANTIN, Dennis
   TITLE OF INFERINGE: MMI100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PATENTIN Version 3.1
; TYPE: NNA
                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Bovine 19866880687880
US-10-750-185-55479
                                                                                                                                                                                           Query Match 16.9%; Score 31.4; DB 6; Best Local Similarity 32.7%; Pred. No. 0.39; Matches 37; Conservative 25; Mismatches 51;
                                                                                       677 TACACAAGATTTCTTTTGTTTATTAAGCCATAGGAATAACGGTGGCCTTTTCC 729
                                         61 UAGUUAAGGUUGCGUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGC 113
                                                                                                                                                                                              51; Indels 0;
                                                                                                                                                                                                                                       Length 1713;
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Gaps

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FILE REFERENCE: MMILIOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 33993
LENGTH: 1825
TYPE: DNA
ORGANISM: Bovine 19866881131067
US-10-750-185-33993
RESULT 4
VS-10-995-561-13259
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 43180
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Matches
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43180, Application US/10750185 Publication No. US20050260603A1
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10-750-185-43180
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 15.5%; Score 28.8; DB 6; Local Similarity 33.3%; Pred. No. 2.7; nes 32; Conservative 22; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                 1044 TGAAAATGGAATAAAACTTTCCTTGAAAATTGGAATCATAAAATCAAACATTCAAAGAC 1103
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; ORGANISM: Homo sapiens
US-11-121-086-54
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(387780)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7 US-10-995-561-13259
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US-11-121-086-54
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CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
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Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559
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Best Local (
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: RastSEQ for Windows Version 4.0
SEQ ID NO 13259
LENGTH: 387780
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 189252
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                                                                                                                                                                   34931 TTTGGCTATTGTTAACCAGTGTTTCTCTTAATATGCATGTTTTGGGTTAATTTCAGGTAA 34990
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Similarity 31.3%; Pred. No. 42;
26; Conservative 23; Mismatches
                                                                                                                       CGCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCGCGUUGCAGUCCAACAAGAUCCAGGG 132
                                   ACUGUACAGAAUUUUCCUAUACCUCGAGUCGGGUUUGGAAUCUAAGGUUGACUC 186
                                                                                                                                                                                                                                                              Conservative
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25.3%; Pred. No. 36;
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US-11-121-086-40/c
Sequence 40, Application US/11121086
Sequence 40, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: NUILESEN, TIM S.
APPLICANT: NUILESEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
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Sequence 39, Application US/11121086
; Sequence 39, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, KIRSTEN V.
; APPLICANT: NIELSEN, KIRSTEN V.
; APPLICANT: NIELSEN, KIRSTEN V.
; FITTLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION UNMBER: 60/567,570
; PRIOR PILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; NUMBER OF SEQ ID NOS: 107
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; ORGANISM: Homo sapiens
US-11-121-086-39
                                                                      US-11-154-865-1/c
                                                                                                   RESULT 8
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LENGTH: 207835
TYPE: DNA
ORGANISM: Homo sapiens
Sequence 1, Application US/11154865 Publication No. US20050251884A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.3
SEQ ID NO 39
LENGTH: 207835
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SOFTWARE: PatentIn version 3.3
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Local Similarity 41.2%;
nes 40; Conservative 14
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                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
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US-10-821-234-22
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CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 22
                                                                                                                                                                                                                                                    Query Match 14.8%; Score 27.6; DE Best Local Similarity 33.3%; Pred. No. 9.9; Matches 46; Conservative 23; Mismatches
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CURRENT APPLICATION NUMBER: US/11/154,865
CURRENT FILLIG DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/10/072,077B
PRIOR FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
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APPLICANT: Stache-Cra
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APPLICANT: Young, Todd E.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Generation of Multiple Embryo Maize
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                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2613
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)...(3183)
OTHER INFORMATION: senescence-associated gene 12-1 (SAG12-1) promoter
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                                        168 UGGAAUCUAAGGUUGACU 185
                                                                                                                          108 CGUUGCAGUCCAACAAGAUCCAGGGACUGUACAGAAUUUUCCUAUACCUCGAGUCGGGUU 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 TATGGGTTCTTCTAATGTT 264
                                                                                                                                                                                                                48 GAAAGUAUUGCUAUAGUUAAGGUUGCCCUUGCCUAUUUAGGCAUACUUCUCAGGAUGGCG 107
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Andarmani, Susan
Tang, Y. Tom
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                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                           69; Indels
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                                                                                                                                                                                                                                                                                                   Length 2613;
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FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3350
LENGTH: 2104
TYPE: DNA
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US-10-793-626-3350
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Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOCTWARE: PATCHLIN Ver. 2.1
SEQ ID NO 1199
LENGTH: 1332
TYDEE. NAS
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publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS
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    1741 TAGT 1744
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RESULT 12
US-10-793-626-3441/c
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APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
FILLE REFERENCE: PUJ480US
FILLE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR PRIOR DATE: 1999-11-09
PRIOR PRIOR DATE: 1999-11-09
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SEQ ID NO 3441
LENGTH: 3153
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 151
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Publication No
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Retter, Warg W.
APPLICANT: Retter, Warg W.
APPLICANT: Panger, Gary R.
APPLICANT: Funger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT FILLING DATE: 2003-07-17
CURRENT FILLING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                     LENGTH: 4655
TYPE: DNA
ORGANISM: Homo sapiens
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                                               2934 AAGTTTTACTGTGTATTAATATTCAGGGTAAATAGGAATCATTCAGAAATGTTGAGGCTCTG
                                                                                                                           61 UAGU 64
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            GUUUGGAAUCUAAGGU 180
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37.5%; Pred. No. 15
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Best Local Similarity
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; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-623-155-335
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Sequence 32, Application US/11121086
Sequence 32, Application US/050266459A1
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES.
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                          SOFTWARE: Patent
SEQ ID NO 32
LENGTH: 160170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 335, A Publication No.
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APPLICANT: Peckham, David W.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: U9/10/623,155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
NAME/KEY: modified base LOCATION: (8540)...(8540) OTHER INFORMATION: a, c,
                                                                             NAME/KEY: modified base LOCATION: (7125)..(7125) OTHER INFORMATION: a, c,
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                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: modified_base
LOCATION: (115733)...(115734)
OTHER INFORMATION: a, c, g,
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LOCATION: (111433)...(111435)
OTHER INFORMATION: a, C, g,
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NAME/KEY: modified_base
LOCATION: (103581)..(103581)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified_base
LOCATION: (102478)..(102478)
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LOCATION: (34208)...(34208)
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NAME/KEY: modified_base
LOCATION: (115727) ... (115728)
OTHER INFORMATION: a, c, g,
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NAME/KEY: modified_base
LOCATION: (103460)...(103460)
OTHER INFORMATION: a, c, g,
                    LOCATION: (115730)..(115731)
OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a,
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FEATURE:
NAME/KEY: modified_base
LOCATION: (152427)...(152427)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (152431)...(152432)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (152589)...(152589)
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LOCATION: (120790)...(120790)
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LOCATION: (121605)...(121605)
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NAME/KEY: modified_base
LOCATION: (121603)...(121603)
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Copyright (c) 1993 - 2005 Compugen Ltd.
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| 34.2 | 34.2 | 34.2 | 34.6 | 34.6 | 34.6 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 34.8 | 35 | 35.2 | 35.2 | 35.2 | 35.6 | 35.6 | 35.6 | 35.6 |
| 18.0 | 18.0 | 18.0 | 18.2 | 18.2 | 18.2 | 18.3 | 18.3 | 18.3 | 18.3 | 18.3 | 18.3 | 18.3 | .18.3 | 18.3 | 18.3 | 18.3 | 18.3 | 18.3 | 18.4 | 18.5 | 18.5 | 18.5 | 18.7 | 18.7 | 18.7 | 18.7 |
| 206214 | 185773 | 166300 | 178453 | 163700 | 802 | 316005 | 248999 | 231876 | 178212 | 172764 | 169768 | 167125 | 165603 | 148705 | 141889 | 132200 | 94924 | 69514 | | 226957 | 200773 | 180201 | 183466 | 181361 | 152842 | 152395 |
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| AC079859 | AC027528 | AC018884 | AC016144 | AC074030 | BV027456 | AC111792 | AC120992 | CR853302 | AC013326 | BX294434 | BX511118 | CR855877 | BX548250 | CR847523 | AC032006 | AL161619 | AL355997 | AY129465_4 | AC132039 . | BX572639 | AL772398 | BX548064 | AP005241 | AC015571 | AC067921 | AL161907 |
| AC079859 Homo sapi | AC027528 Homo sapi | | AC016144 Homo sapi | AC074030 Homo sapi | BV027456 S212P6024 | | AC120992 Rattus no | N | AC013326 Homo sapi | BX294434 Zebrafish | BX511118 Danio rer | CR855877 Danio rer | BX548250 Zebrafish | CR847523 Danio rer | AC032006 Homo sapi | AL161619 Homo sapi | AL355997 Human DNA | Continuation (5 of | AC132039 Rattus no | BX572639 Danio rer | AL772398 Mouse DNA | BX548064 Zebrafish | AP005241 Homo sapi | AC015571 Homo sapi | Нопо | AL161907 Human DNA |

ALIGNMENTS

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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BD173516
LOCUS
DEFINITION
                                               ORIGIN
                                                                                                                                                                                                                                                       COMMENT
                                                                                                         FEATURES
Query Match
Best Local Similarity
Matches 134; Conserv
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                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                              source
                                                                                                                                                                 1 (bases 1 to 190)
Nakashima, N. and Kanamori, Y.
Novel tertiary structure having ability to accelerate translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BD173516 190 bp Novel tertiary structure having
                                                                                                                                                                                                                                                                                                                                                                                         unidentified
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WO 02061080-A/6.
                                                                                                                                                                                                                                                                                                                 activity
                                                                                                                                                                                                                                                                                                                                                                  unclassified.
                                                                                                                                                        translation activity
                                                                                          /organism='Black queen-cell virus'
Location/Qualifiers
1. .190
                                                       /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
100.0%; Score 190; DB 70.5%; Pred. No. 3e-45; tive 56; Mismatches
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA linear PAT 18-FEB-20 ability to accelerate translation
                       DB 6;
                      Length 190;
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BD177020
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JP 2002306168-A/6.
unidentified
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                                                                                                                                                                                                         CAAUUUACCU 190
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                                                                                                                                                                                                                                                                                                                  CAATTTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
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AF183905
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leat, N., Ball, B., Govan, V. and Davison, S.
Analysis of the complete genome sequence of black queen-cell virus,
a picorna-like virus of honey bees
J. Gen. Virol. 81 (Pt 8), 2111-2119 (2000)
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Black queen cell virus
Viruses; seRNA positive-strand viruses, no
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structural polyprotein
AF183905
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SFLSYVIPPLFLESVVDTKSNLFKRIMKSKDLDLDLVVRKLSYFGDAKIYNAFDNIGTML
TTMINKTVNYVKVTLLGHIDESEPLBNQSDEPLDWEGDCCKHFVSDTDRIAIYTESTLA
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YGETGVGKSTLTYPLCATLLKTIFTREGONTWLESLKCHYKKENIYVRAABQEFNDGYT
QQLVTVFDDDRANQVDSSANESLELFEIIRSSNIFPYPLHMASIEEKANTVFQSKVILC
SSNNKTPKTESLNYFKALLRRFAKFVENKRAPSESGTFSTDCYTFVEYDFFDHCNIVK
SMSFNELLIDEVVAMYFHEGEFVSSVDKFIMENVFAQGGGSLSDBEEDDFTEASSYGDSN
LDEALTREEKKEIIRCINDGFKNENDTTSFQLIRVFHCAKDSLQEKFLAYRRKYSF
DDWFSFSKASKVTLGILSLYLVGYGIYSYVKGNPAKNTRTWSSBEVIIHNSLIEKGDDI
VQSEACSDINASEQLTAVTTNNTYYMTILSKESVIRVGHCIFLKGKIAVAPGHYLRIL
QRAYELDDGAILGPHHPYGKRNEFFIGDIGFSLYKKNTTWRSSBEVIIHNSLIEKGDDI
VQSEACSDINASEQLTAVTTNNTYYMTILSKESVIRVGHKITKNGGGGTSCIKNVSNVS
MTDTDPDAREIRLREAMEYSLETISGDCGAPLFVTNSKGPGKIIGHFFVDK
SVYHRDISSYFCERLELGSVGSTRIQLEVMRWRDDVSIFFDACKY
SVYHRDISSYFCERLELGSVGSTRIQLEVMRWRDDVSIFFDACKILDHFFIDTKAD
SCATFPYLBDVKGTLSKTDVXGQSAPTWLYFRELDGQIFDLKYRTALGKDVSVPIRS
KLINLAWALIDDIYSVYLQKKOLLDGAFPSSLTFDQAVLGIFGCTPLKMGXVKD
PPVQBSRSKISPSPLKGHITEPSSAPTWLYFRELDGQIFDLKYRTALGKDSVPIRS
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ARYLKSSCHHWAGDDFGFDASEGSDILYAAGSTLUHYFDDTLADG
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FFRECGIVAYGDDHVVSVPEKYLSVFNQQTLPVLMSKFGMFYTIETKDDTEIDFLSRR
LEDVSYLKRNFVYDESRQRYIAPLSLDVVLEMPMMTKSSKDIVTNVFCNLEHALKELS
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/mol type="genomic RNA"
/strain="South African"
/specific host="Apis mellifera"
/db_xref="taxon:92395"
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/codon_start=1
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VERSION
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BD173514
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Best Local
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Patent: WO 02061080-A 4 08-AUG-2002;

JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

TOS Cricket paralysis virus
PN WO 02061080-A/4
PD 08-AUG-2002
PF 31-JAN-2001 WO 707-7
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BD173514.1 GI:28414845
WO 02061080-A/4.
Cricket paralysis virus
Cricket paralysis virus
Viruses; seRNA positive-strand viruses, no
Dicistroviridae; Cripavirus.
1 (bases 1 to 188)
Nakashima,N. and Kanamori,Y.
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FLKSGANWVSENILQPADEI 1GPILSLFGFSKELLP I INPTVLREANIFA I TDYNDMS
HSLALLSNDTMVPFVKALDGSCLEMSFDYLKKI PQFTOS KFFTTTTROBEVLFQTKW
HYFVPAGDVTVAMDKOKTRTI WQPSHLAYI TSMFKYWTGSLVYTFKFVKTDYHSGRV
E1 SFHPFSDYTANSYSDYTKRI I VDLÆKSEFSVTL PFI SPVFYKRI SR.DDWDKPYSK
YAHASTGTLVLKALTSLKATNTVVSNSVEIL I EVNAGDDFNVI AP I ENIF FPFSLSPG
RKGMVAQSNSGTEQQNERGSSLLTDESSI TKSDFYNPNI SLLI SGEVFTNFRNLI KRV
NFRKATTLNGKRI SDTFDINSLI EAPRLDI AQVDTERKÆAKFGS YFWSAFTTLNIV
NFRKATTLNGKRI SDTFDINSLI EAPRLDI AQVDTERKÆAKFGS YFWSAFTTLNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAEQINENYENKQQLVEQTEITTEENDLIVLEDGPQMEEPLPYAFHGQPTDHYNAFTUVNFLQRPQVIFDSSWASDLPRNYENYENTWEATHVSETHLNHKHKERLLLHNYENGKSSLRATNUTVQNFLQPFQAFWLGSFPLFTLHFTNYEATHVKEATHNHSHKLLHNYENGKSETHNHSKERLLHNHYGGFPGAFWLGSFPLFTHFTNYEATHNHSKETHLLHNYGGFPEDCDIAKETEVSLRIPFVSPYNSYDLVSKRPPWAKVVGLVYSPLTTTIPVDYIVYGHFEDCDIAKETEVSLRIPFVSPYNSYDLVSKRPPWAKVVGLVYSPLTTTIPVDYIVYGHFED
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AEFQIPYYAPCLSSSFRANSETFYYSSGRNNLDIATSPPTVNRYYAVGAGDDMDFSIF
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likely facilitated by an internal ribosome entry site
(IRES); a region similar to Plautia stali intestine virus
IRES was identified immediately upstream of orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_except=(pos:5834. .5836,aa:Met)
/product="structural polyprotein"
/protein_id="AAF72338.1"
/db_xref="GI:8100532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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70.5%; Pred. No. 1.9e-45;
tive 56; Mismatches 0
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having
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                                                                                                                                                                                                                                                                                                                                                 Cricket paralysis virus
Cricket paralysis virus
Cricket paralysis virus
Cricket paralysis virus
Viruses; saRNA postitive-strand viruses, no DNA stage;
Viruses; saRNA postitive-strand
1 (bases 1 to 188)
Nakashima, N. and Kanamori, Y.
Novel translational activity-promoting higher-order structure
Patent: JP 2002306168-A 4 22-OCT-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND
ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION
ORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND
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BD177018
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                                                                                                                                                                       OS Cricket paralysis virus

PN JP 2002306168-A/4

PD 22-OCT-2002

PF 25-CAN-2001 JP 2001016746

PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N15/10,C12P21/02// PC

(C12N15/09,C12R1:92),C12N15/00,C12N5/00,C12R1:92) CC

(Novel translational activity-promoting higher-order structure FH

Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP 2002306168-A/4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACAATATCCAGGAAGCCCTCTCTGCGGTTTTTCAGATTAGGTAGTCGAAAAACCTAAG 178
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                                                                                                                                                            Bource
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C12N15/11,C12N15/86,C12P21/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       018 translational activity-promoting higher-order structure
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                                                                                                                /organism='Cricket paralysis virus'
Location/Qualifiers
                                                   <u></u>
                                                                     /organism="Cricket paralysis
/mol_type="genomic RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Cricket paralysis virus"
/mol_type="genomic RNA"
/db_xref="taxon:12136"
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                                                     xref="taxon:12136"
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42.7%;
 33.4%;
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Pred. No. 7.5e-08;
3; Mismatches 61
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Score 63.4;
   DB 6;
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 Length 188;
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Submitted (20-DEC-1999) Microbiology & Immunology, Stanford University, 299 Campus Drive, Stanford, CA 94305, USA Location/Qualifiers
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Wilson, J.E., Powell, M.J., Hoover, S.E. and Sarnow, P.
Naturally occurring dicistronic cricket paralysis virus RNA
regulated by two internal ribosome entry sites
Mol. Cell. Biol. 20 (14), 4990-4999 (2000)
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Cricket paralysis virus
Criuses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
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Cricket paralysis virus nonstructural
polyprotein genes, complete cds.
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DDLKGAKGEVQQLNGNLTRICOPLENGLPTLFAQIQTVLITTDKYVNLKEDLLKVAI

LLVLVRLLMYMKKYRAALIVIILFVMHFYGFDXQILDIVLDLKDLIQTTQAGTETL

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KWSKMWTILDEQISALSTKIRELKNKAYKFISHHPYLTALGFIGWNISAFAWYSFFER
KUNDNTTTGEVGSGCGTNUKTOVIGKENDHOOG
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VVPVSHFIAPNAERVELTTACTRIHYKDETPRDCVLVNLHRRMCHPHRDILKHFVKKS
                                                                                                                      TLTDDTITSEVGSSGDNKTQKISKRVVEVGGSGDVKTTKPAKTAVEVGSSGDSKTMKN
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/protein_id="AAF80998.1"
/db_xref="GI:8895507"
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DQGNLEGVEQOTLATTHQSANELCRAYQMLQAIRPLDQEITIYHEDTDMFDYESESYT
ORDCYEYNAPTQTGNCGSIVGLYKKRMEKLIGHAIPRUNGECHGYACPLTQEAIMOG
LNRLEKLDPUNNITYGCCEPEPSDIKOTMSGETPEGKFCALIGKSNIKVGQAVKTTLLK
SCIYGMLSKPITKPAHLTRTRLPNGEIUDEMKGLKCGVUDTAVLDAEIVESAALDVK
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HSVHSYGDNVCLNISDRVUEMFNQITISEQNKEIKHMILADERVPDF"
HSVHSYGDNVCLNISDRVUEMFNQITISEQNKEIKHMILADERVPDF"

**CE217...8904

**CC4217...8904

**CC4217.
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δ Ś 밁 밁 문 S В S Matches Query Match Best Local 6207 8809 6147 6029 182 122 62 N 79; Similarity AAATT 6211 AAUUU 186 CUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAAC 181 CTATTTTTGTATTTAGGTTAGCTATTTAGCTTTAGCTTCCAGGATGCCTAG-TGGCAGCC CUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCC CAAAAATGTGATCTTGCTTGTAAATAC-AATTTTGAGAGGTTAATAAATTACAAGTAGTG CAACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUG CCACAATATCCAGGAAGCCCTCTCTGCGGTTTTTCAGATTAGGTAGTCGAAAAACCTAAG 6206 Conservative 33.4%; 43; Score 63.4; DB 13 Pred. No. 4.6e-08; 3; Mismatches 61 13; 61; Length 9185; Indels 2 Gaps 6146 6087 121 61 Ŋ

REFERENCE AUTHORS RESULT 7 AR496112 LOCUS VERSION KEYWORDS FEATURES SOURCE DEFINITION ACCESSION JOURNAL ORGANISM Sequence AR496112 Drosophila sequences
Patent: US 6703491-A 1072 09-MAR-2004;
Exelixis, Inc.; South San Francisco, CA
Location/Qualifiers 1 (bases 1 to 1345)
Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buch Unclassified Unknown. Unknown AR496112.1 GI:52431587 AR496112 1072 from patent 1345 bp DNA t US 6703491. Buchman, A.R. linear Francis-Lang, H.L., PAT 22-SEP-2004

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1345)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R. Drosophila sequences
Patent: US 6703491-A 16354 09-MAR-2004;
Exelixis, Inc.; South San Francisco, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUU 66
BD173513 189 bp RNA linear PAT 18-FEB-20 Novel tertiary structure having ability to accelerate translation
                                                                                                                                                                                                                                                                                                   7 AUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUU 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16354 from patent AR511394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
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                                                                                                                                                                                                                                                                      ACC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAAUUU 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTGATCTTGCTTCCTTATAC-AATTTTGAGAGGTTAATAAGAAGGAAGTAGTGCTATT 581
                                                                                          AAC
                                                                                                                        ACC 189
                                                                                                                                                                                                                                                                                                                                 Conservative
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/mol_type="genomic"
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                              24.7%;
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                                                                                                                                                                                                                                                                                                                              Score 47; DB 6; Length 1345;
Pred. No. 0.0041;
42; Mismatches 70; Indels
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                 PAT 18-FEB-2003
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BD177017
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ORGANISM
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Best Local
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                                                         TITLE
                                    JOURNAL
                                                                          AUTHORS
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BD173513
BD173513.1
                                                                                                                     BD177017

Novel translational activity-promoting higher-order structure.
BD177017

BD177017.1 GI:30014277

BD1002306168-A/3.

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus

Drosophila C virus
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JAPAN AS REPRESENTED BY DIRECTOR GENERAL OF NATIONAL INSTITUTE OF
SERICULTURAL AND ENTOMOLOGICAL SCIENCE MINISTRY OF AGRICULTURE
FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 189)
Nakashima, N. and Kanamori, Y.
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Drosophila C virus
Dicistroviridae; Cripavirus.

1 (bases 1 to 189)

Nakashima, N. and Kanamori, Y.

Novel translational activity-promoting higher-order structure

Patent: JP 2002306168-A 3 22-OCT-2002;

PATENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMOTION
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                                                                                                                                                                                                                                                                                                                                                                                                                   ATATCCAGGACACCCTCTCTGCTTCTTATATGATTAGGTTGTCATTTAGAATAAGAAAAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAATAATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCTAT-TGGCAGCCCCATA 124
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25-JAN-2001 JP 01F 016746
NOBURIKO NAKASHIMA, YASUSHI KANAMORI
C12N15/11,C12N15/86,C12P21/02
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WO 02061080-A/3
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/mol_type="genomic RNA"
/db_xref="taxon:64279"
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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ACCESSION
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AF014388
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Johnson, K.N. and Christian, P.D.
The novel genome organization of the insect picorna-like virus Drosophila C virus suggests this virus belongs to a previously undescribed virus family
J. Gen. Virol. 79 (Pt 1), 191-203 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                         Submitted (16-JUL-1997) Entomology, CSIRO, Clunies Ross Canberra, ACT 2602, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Drosophila C virus
Drosophila C virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
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Drosophila C virus strain EB,
AF014388
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                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                 2 (bases 1 to 9264)
Johnson, K.N. and Christian, P.D.
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OS Drosophila C virus

ON JP 2002306168-A/3

PD 22-OCT-2002

PF 25-JAN-2001 P2001016746

PF NOBUHIKO NAKASHIMA, YASUSHI KANAMORI

PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/0

PC C12N15/09, C12R1:92), C12N15/00, C12N5/00, C12R1:92
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22-CCT-2002
25-JAN-2001 JP 2001016746
25-JAN-2001 JP 2001016746
NOBUHIKO NAKASHIMA,YASUSHI KANAMORI
C12N15/09,C12N1/15,C12N1/19,C12N15/10,C12N5/10,C12P21/02// PC
C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC
N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC
1 translational activity-promoting higher-order structure FH
Location/Qualifiers
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                                         /db_xref="taxon:64279"
799. .6078
note="includes putative protease, helicase and RdRp lomains; putative; ORF-1"
                                                                       /organism="Drosophila C virus"
/mol type="genomic RNA"
/strain="EB"
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/mol_type="genomic RNA"
/db_xref="taxon:64279"
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CDS

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67

6143 TTAATAATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCTAT-TGGCAGCCCCATA 6201

GUUGGAAUCACCGUACCUAUUUAGGUUUAACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUC 126

127 AAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAAUUU

6084 ATGTGATCTTGCTTATAC-AATTTTGAGAGGTTAATAAGAAGGAAGTAGTGCTATC 6142

AUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUU 66

Indels

2

Gaps

2;

ORIGIN

Matches Query Match Best Local

Conservative

7 69;

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Similarity
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DLSHVLSI PNEWBTEFWNITDATSSILMDNYVTPMKI KPYSSTILDRERCTHMGFVAN
THGKWAGSI TYTFKEYKKTQEHSGRLALSEI PEYVNITTISAGVEDVSRTQKVITVLLTS
TEVSFTIPYVSSRPMMYCIRPEÄSMLGTDNALMYNAVTGIVRVEVLNQLVAANNVFQS
DTIVEVSGGFDLIFFAAPMABSYVPYSGFTLADDAAAKKQREESYDNNIPQTISNIRG
KREVEDDARIVAQVMGEDLALQRUDAGHGVHENTLDTHKIDSNWSPEAHGIGEKLMSIR
QLIKREGMALNSLALISDAPNTLIAPFSVQHPTPVVAPAEPMSLFEYYYFIYGFWRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="ANFQTNNNNIENEDRKITSEQKEIVHFSSEGVTPSTTAVPDIVS LSTDYLSMTTREDRHTIKDFLSRFIIIQTGLWSSATTAETQLYANFPEVFISNTMY OEKLRGFVGLAATLVIKVQVNSQPFQQGRLMLQYYPYAQYMPNRVSLVNSTLQGRSGC PRTDLDLSVGTEVENRIFYVSPHVYYNLITGQSFGAIYLVYVSQLRDQVTGTGSVEY TVWAHLEDVDVQYPTGANIFTGSSPHYXVNLITGQSFGAIYLVYSQLRDQVTGTGSVEY TVWAHLEDVDVQYPTGANIFTGSSPHPASLGQMSDGKFTEKDLRDIWTSKAYNKQPD KIFAQVASEITQLKESGTISSGIGQVSEGLSTMSKIPILGNMFTKPAMISAQVSNIFK
                                                                                                                                                          IVAVAPQGTIATTDVVNAQFARAPSDDFSFMYLVGVPPLTNVARP"
                                                                                                                                                                                MRFKLQAVRTNSAETSVKTDTTWTVNLMNSVQDSFNSLINVFSTTDYPIKSTGALPAG
TSGF¢NSMTYIDÞEVEGFMEFEIFYYNISHISPATTYVRGTESPITINSVLRGHLPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSLVAQILMAIFWEIFVVMLKQFIDIENSEGKRILCICLGLMSHLVHSVHIYEDNVYM
WTHSQPSGNPFTVIINCLYNSIIMRLSWIRVMEKFQPRLKSMKWFNEYVALITYGDDN
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PVYYRYDDRYTRLEKAIERDDKIKTLIKELARQIKGRKIYSQGMFDKLTKQISDGI
KDGVQSEQMKOLTRICOFLENTLPGLQANIQATVIDTDKYVSLKEDIMKIVLVLL
VRLLMVWKKYRASLCVILIFIRKPYGFDQKLIDLIMDLKNKIFSQGALBDTVEEVVYH
PWFHTCGKIIFAVMAFLTIKKIPGKQDWDSYITRLDRIPKSIEGAKKITDYCSBYFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="capsid polyprotein"
/protein_id="AAC58808.1"
/db_xref="GI:2388674"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKVPQELPENPQILTYNQYLHDIEYLADPLYDF"
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LQRHVAPLKIEVIYEMLNWSRRSIDPDBILMSNIETAFREVVYHGKEEYDKLRSAVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF-2; putative; translation start site unknown"
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/product="replicase_polyprotein"
/protein_id="AAC58807.1"
/db_xref="GI:2388673"
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23.9%; Score 45.4; DB 13; 37.7%; Pred. No. 0.0096; tive 41; Mismatches 71;
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the rise found the longest good mailty representation will be here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 1, 2005 this sequence version replaced gi:61969306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence.
BX569779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 182464)
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                                                                                                                                                                                                      VECTOR: pTARBAC2.1
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                                                                                                                                                                                                                                               //www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-11319
                                                                                                                                                      1. .182464
                                                                     /mol_type="genomic DN
/db_xref="taxon:7955"
                                                                                                                           'organism="Danio rerio'
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                                                                                                                                                                                                                                                                                                                                                       assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found the WORMPEP database can be found thtp://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone, and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 9, 2004 this sequence version replaced gi:45772220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                       Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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1 (bases 1 to 30205)
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CR318586
                                                                   lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtmlCH211-239022 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                  submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: zfish-help@sanger.ac.uk
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Location/Qualifiers
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Pred. No. 1;
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organism="Danio rerio"

_type="genomic DNA"

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JOURNAL
PUBMED
REFERENCE
AUTHORS
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AUTHORS
TITLE
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KEYWORDS
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AB017037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10550677
2 (base
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35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-AUG-1998) Nobuhiko Nakashima, National Institute of Sericultural and Entomological Science, Department of Insect Physiology and Behavior; 1-2 Owashi, Tsukuba, Ibaraki 305-8634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 9275)
Nakashima, N. and Sasaki, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakashima,N., Sasaki,J. and Toriyama,S.

Determining the nucleotide sequence and capsid-coding region of himetobi P virus: a member of a novel group of RNA viruses that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Himetobi P virus
Himetobi P virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB017037 9275 |
Himetobi P virus genomic RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:81-298-38-6028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan (E-mail:nakaji@nises.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dicistroviridae, Cripavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein precursor; capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB017037.1 GI:3493357
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             TIVLSWNEVCESMSVERMVAVCECAREQGIFNVSLGINDDTKGYIDSVVSRIGNGVCS
LYTDTMLGLEVAASDILVNLKYIVGFLVAAVLVGVATYCGVKMISKLEPRFESLVFKS
DESMMVAAQQGSGDTWNGFLMLLMSVFGVSAGALKSARCMNAIRCISMLFRAEGGID
TIFTWIKSTYTMCYRIFSKYVLGVDFGVGVSAGALKSARCMNAIRCISMLFRAEGGID
TIFTWIKSTYTMCYRIFSKYVLGVDFGVQVSADSHFVASWILEELGEFYKSFSNGTFSY
DSATFSIHHSLFIRGLMLQRSSFFRSDQIAIRTGMDCLMKLITEERSRNIEAGSVRNP
PVVIYLHGGSGGKSTLTNVLAASILSKIQFDMNLKKQGKNLIYSRASGFFWDGYTG
QLVTVFDDFSQRADSAGNENVELFDIVRAANVYEYELHMANLSDKASTNFTSKIIICS
SNLKQFKTESLNFFNALYRRFDVCVSVSKNEKYNDVPTHFVEDFYQFQEYDMLKKED
LGSTDWEGIVDKCYELYKHRSDFVSSLDEKIQEILGSTQFEDVPLNVAQFQVNCDYLG
FCNCDCWGSTMCVNTNLHQFKWKQWLLKMKHYVTGIFKGSVYBAFEKMFLSQSYLLNA
SKSRFGRWLTSIKERFPVIKDLRIHLTVATVVMGPMVFFGVKGLFAKKNECVELHFYS
ESYDVGNIKFTREYETENVEFTKTESYESPNVKSVKTESYESSENVKFVRAKGSFPS
STONGONIKFTREYETENVEFTKTESYESPNVKSVKTESYESYBSPNKFVRAKGSFPS
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DCQIALYYMTRVLYDAKVCSRRVRRTAYALCRILNHVPEHLIPYINKDLIENFELCVP
FRRKLVMYLLKRCLLFSDLPLEIRWKDYCYDERNYEEKIEEVQEQVFNVASQSRSDIE
                                                                                                                                                                                                                                                                                                                                                                                     /product="nonstructural protein precursor"
/protein_id="BAA32553.1"
/protein_id="BAA32553.1"
/db_xref="G1:3493358"
/translation="MSQLIQTKISSYKNYVNQKIKEGRSNIHPLLRATPNFVEDVESD
/translation="MSQLIQTKISSYKNYVNQKIKEGRSNIHPLLRATPNFVEDVESD
LKNLNEAIRTTDVFKNYVDELTIGHQDLDFGYFKLYNRDLENLVYSMTSMNETHLHPD
LKNLNEAIRTTDVFKNYVDELTIGHQDLDFGYFKLYNRDLENLVYSMTSMNETHLHPD
GRVSGSEMNLASLQLDNYIKEVKEQGVSDQNAAEICSKLVTKNMFKIYVENDHVSIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic RNA"
/specific_host="Laodelphax striatellus"
/db_xref="taxon:81583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Himetobi P virus"
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/clone="CH211-239022"
/clone_lib="CHORI-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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; Pred. No. 1.7;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9275 bp RNA linea: RNA, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel:81-298-38-6109
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CCTGCAATATCCAGGGCACCTAGGTGCAGCCTTGTAGTTTAGTGGACTTTAGGCTAAAG
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LITTIDIEDDLMTSMYYDKLJGFATEKADTIERVQVNAQPEQCEKLVNAYIRWEDSIAS
TETAELTRAIDRI IALPHVQLDISEQSEVTLRVEYISEYSAYNLIEGRYRWGRVVVAV
YSPLNQVSQENLKVNIFGYYDNVTLGYETLGTIALSEVAVAREQVNLNSEADMIRIAE
YSPLNQVSQENLKVNIFGYYDNVTLGYETLGTIALSEVAVAREQVNLNSEADMIRIAE
SRNFFTKIAASINGVIQKGSDILGNVLPQTKSFTNEVAKISDAAFDIISMIPGFKKPD
KTNHGETVLFRETQYFGNVDGVEHSHKLGYHANNRIDFQDEFRASKMDEMSFDYVKRI
ENYLDSFSYSNSNVYGDTLMSTAVSEGYFSHDFINDAVBTTRGEPTPTSLTYAIGFSE
LWRGSIVYTFRAVKTEYHSGRIEFSFNPFINLDMYNTNKTTRSEYVYKVILDLRTQTE
ISFTVEYAGTTFFKAIRFEISFLSSSGISVDDFNVFATGVLGVAFATTFELVLGSTVUFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIQILVEMKGGPDFEVECPNSTGMMPIHSITPAATGRDTVDSELVSTAQEQANFASTG
QHDIRSDYLEDKIEIKDITGISSNISLNTEKSLSCVGESFGNFRDLIKRFGMFKNQSV
AFTNTKILSGIPIVNYTSSIAGTGLTLTADGGSTPLTMVSSMYAFFRGGFRAKVYIHD
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ESPEPTESLASSRDLCSFCLDNTINFSDVSKLFVSKSDLSLKSSDILLPTLSTPSNG
QAFAKIKIGRAASGIQRQDCRVYGSDPTDRLRLVRYCMFXVLETEVGDCAPLIANU
ALAGRKIMGHHIAGNTDAGFSTPLYKEDIDTILSMYPLESQVANEQCQPTHMPTGCHL
PESTSFVVLDKIEKPLYASSKSVISPSPLHGILTTPKTKPCQLRDTPEFSPMQYRLEK
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NSVKRSSSPGYPFVFDKEWNSKEKIFGKGPEFDVTNEKAILLRQQVEEIISQAKLGVR
QQHVFIDTLKDERKPIHKAHKTRMFSACPLDYLIACKMYFGGVVSLLQKSRNICGISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSYGFVTSPLRVDPFDKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAGEMVQGALI DNSQNTNVPQPLALQSLQYELSDKRLYEFSWPYYCPTYLTTYPSGS
LNY I SDLVNPTTYAR I TTI SEYATAYAMAAADDFDCGFYLGAPLSWNWE I ERLAGRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     upstream codon,
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ATVNAPYRSLNEVSYLKRKFLWDEDKRQYLAPLSLETILETPMWVKKCVDVNLQTTTE
LENSLKELCLHPQSVWDSHIESFKHCAKLLGSFPLFLDREFARSFVLNENV"
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EEDLLVMQVLLESLLSSVHLNNNYVYMWLKGLPSGHFLTAIINSIFVLISFNSVWQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="ANNNNNNNTNSQKVNDTTFSDRENPSVSAGRIDESVEFTQEIT"
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/product="capsid_protein_precursor"
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/db_xref="GI:3493359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="translation is supposed to start at several upstream codon, directed by Internal ribosome entry site
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                                                                                                                                   DEFINITION
                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                         KEYWORDS
                                                                                                                                                    Snoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                     6403
                                                                                                                                                                                                                             6463
                                                                                                                                                                                                                                                                                                                                              6345 CTACATTTTAAGACCCTTAGTTATTTAGCTTTACCGCCCAGGAT--GGGGTGCAGCGTT 6402
                                                                                                                                                                                                                                                                                                                                                                                                        6285 CGAAAATGTGTGATCTGATTAGAAGTAAGAAATTCCTAGTTATAATATTTTTAATACTG 6344
                                                                                                                                                                                                                                                       182 AAUUUACCU 190
                                                                                                                                                                                                                                                                                                                122 CUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAAC 181
                                                                                                                                                                                                                                                                                                                                                                          62 CUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCC 121
                          Himetobi P virus
Himetobi P virus
Viruses, seRNA positive-strand viruses,
Dicistroviridae; Cripavirus.
                                                                                                                     AB183472 9275 |
Himetobi P virus genomic RNA,
AB183472
Nakashima,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CAACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                       AB183472.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                             AATTTCACT
                                                                                                                                                                                                                           6471
                                                                                                       GI:50251148
 Kawahara, N., Omura, T.
                                                                                                                    and Noda, H.
                                           no DNA stage;
                                                                                                                                                   VRL 13-JUL-2004
                                                                                                                                                                                                                                                                                     6462
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TITLE

ORIGIN

Matches

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JOURNAL
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spherical viruses isolated from the brown planthopper, Nilaparvata lugens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 9275)
Nakashima, N. and Noda, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax:81-29-838-6028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPEPTESLAESRDLCSFCLDNTINFSDVSKLFVSKSDLSYLKSSDILLPTLSTPSNG
QAFAKIXIGRAASGIQRQDCRVYGSDPTDRLHJVXYCWRYLLETSVGDCGAPLIARNV
ALAGRKIMGIHIAGNITDAGFSTPLYKEDIDTILLSMYPLESQVANEQCQPIHMPTGCHL
PESTSFVVLDKIIKFLYASSKSVISPSPLHGILITTFKTKPCQLADTPESSPMQYRLEK
FASPCVPVDARMLENSVSAVSNHLCKSILENKDLITTSDKSRYSFEBAVSGIDEEFI
NSVKRSSSPGYPFVFDKEWNSKEKIFGKGPEFPVTNEKAILLROQVEEIISQAKLGVR
QQHVFIDTLKDERKPIHKAHKTRMFSACPLDYLIACKMYFGGVVSLLOKRRNICGISV
GTNVYSYDWTIIANTLLSKSPCMIAGDFEGFDSQLQDILRAASQVLLAVSRDMLGST
EEDLLMQVLLESILSSVHLNNYYYMMLKGLPSGLFITAINSIFVLISFSSVMQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNIKOPKTESINFPNALYRRPDVCVSVSKNEKYNDVVPTHFVEDFYQFQEYDMLKKED
LGSTDWEGIVSKCVELYKHRSDFVSSLDEKIGELIQSTDWEDFUNVAGEVNCDVLG
GCODWEGTWOVTMINDPKWKOMLKWKHYVTGIFKGSVYEAFEKWRFLSGEYLNG
EKCHCOWGETWCVMTMINDPKWKOMLKWKHYVTGIFKGSVYEAFEKWRFLSGEYLNG
SKSRFGRWLTSIKERFPVIKDLRLIHLVVATVVMGPMVFFGVKKLFAKKNECVELHVS
ESYDVGNIKFTRTESYEFPVIKDTKTESYESPNVKFTKYESYESPNVKPVRVEWSFPS
GRVSGGEMULASIQLUNYIKEVREGGVSDQUAABAICSKLVTKNMFKIYVELDHVSIFF
GRVSGGEMULASIQLUNYIKEVREGGVSDQUAABICSKLVTKNMFKIYVELDMYIFKVKFF
GHVLFIKGRIAIMPHHFLAALKKFKEQHEGGVVYFRNLFLSRAFFYKLEDMIRKVKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLILSWNEVCESMSVERMVAVCECARROGLENVSLGINDDTKOYIDSVI SRIGNGVCS
LYTDTMLGLEVAASDILVNLKYI VGFLVAAVLVGVATYCGVMISKLFNFFLSLVFKS
DESMMIVAGEOSSDDTMNGPLMLLMSVFGVSAGALKSARCMNAIRCIGNLERAESGID
TIFTMIKSTYTMCYRIFSKYVLGVDPGVQVSADSHPVASWLEBLGEPYKSFSNIEAGSVRNF
PVVIYLHGGSCVGKSTLTNVLAASILSKIQPDMNLKKQWKNLIYSRASEGEFNOGTFSY
PVVIYLHGGSCVGKSTLTNVLAASILSKIQPDMNLKKQWKNLIYSRASEGEFNOGTFO
QLVTVFDDFSQRADSAGNPNVELFDIVRAANVYPYPLHMANLSDKASTNFTSKIIICS
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LYMNILEVYMNENKDI.DI.LGGBNDSWDQYVLSRQLKEMBA.IWGLOAGNVDFII.DTVNP
DCQIALYYMTRVLYDAKYCSRRVRTTAYALGRITLINHVBEHLMBY INKDI.IENFBLCVP
FRRKI.VWYILI.KRCILIFSDMPLEIRWKDVCYDERMYEEKIEEVQEQVFNVASQSRSDIE
SRNFPTKVÄASINGVIQKGSDILGSVLPQTKSVSNPIAKISDAVFDIISMIPGFKKPD
KTTHGETVLVRPTQYFGNVDGVBHTHKLSYHAMRIDFQDPFAGSKMDEMSPVYKRI
PNYIASFSYSNSNVYGDTLMTTAVSPCYRSADVTTTNGARNESFPTPTSLTYALGPFS
LMRGSIVYTFRAVKTEYHSGRIBFSFNPFINLDMYNTNKTTRSEYVYKVILDLRTQTE
                                                                                                                                                             LLTTIDIPDDLMTSMYYDKLDGFATFKADTIFRVQVNAQPFQCGRLVMAYIPMPDSLS
TRTAELTRAIDRIIALPHVQLDISEQSEVTLRVPYISPYSAYNLIEGRYRWGRVVVAV
YSPLNQVSQPNLKVNIFGYYDNVTLGYPTLGTIALSPVAVAREQVNLNSEADMLRIAE
                                                                                                                                                                                                                                                                                         /translation="annnnnnnntnsqkvndttfsdrenpsvsagridesveftqeit
Hfadnapvidssiagetnikpslvtdfhdnrqhsvisflqrpqliktvewapgtaqgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="translation starts at GCU (alanine) triplet,
directed by internal ribosome entry site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGVNVKKAFEFFEVCGIVAYGDDHIVSVPEWATNVFNQYELASLFKQIGLSYTLEDKD
ATVNAPYRSLNEVSYLKRKFLWDEDKRQYLAPLSLETVLETPMWVKKCVDVNLQTTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENSLKELCLHPQSVWDSHIESFKHCAKLLGSFPLFLDREFARSFVLNENV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="nonstructural protein precursor"
/protein_id="BAD27584.1"
/db_xref="GI:50251149"
                                                                                                                                                                                                                                                                                                                                                         /product="capsid protein precursor"
/protein_id="BAD27585.1"
/db_xref="01:50251150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSQLIQTKISSYKNYVNRKIKEERSNIHPLLRATPNFVEDVESD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      country="Japan:Shimane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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lab_host="Nilaparvata lugens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type="genomic RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              start-1
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Query Match
Best Local
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                                                                                                                                             AAUUUACCU 190
                                                                                                                                                                                                                                                                                  CCTGCAATATCCAGGGCACCTAGGTGCAGCCTTGTAGTTTTAGTGGACTTTAGGCTAAAG 6462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTACATTTTTAAGACCCTTAGTTATTTAGCTTTACCGCCCAGGAT--GGGGTGCAGCGTT 6402
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AATTTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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LNYISDLVNPTTYARITTISEHATAYAMAAADDFDCGFYLGAPLSWNWEIERLAGRLD
SSYGFVTSPLRVDPFDKV"
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AFSNTKILSGIPIVNYTSNISGTGLTLTADGGSTPLTMVSSMYAFFRGGFRAKVYIHD
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Pred. No. 2.2;
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Search completed: December 22, 2005, 11:33:59 Job time : 1503.29 secs

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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
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seq length: 2000000000
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1: geneseqn1980
2: geneseqn1990
3: geneseqn2000
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Gapop 10.0 , Gapext 1.0
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190
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Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqn2001as:*
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geneseqn2003as:*
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geneseqn2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | ი | ი | ი | ი | ი | Ω | | ი | ი | ი | | | | | | | | | Result |
|---------------------|--------------|----------------|----------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------|--------------|---------------|--------------|---------------|---------------|---------------|----------------|----------------|--------------------------------------|
| 9 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | თ | IJ | 4 | W | N | ۲ | ult |
| 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 31 | 31 | 31.2 | 31.6 | υ u | 37 | 37 | 45.4 | 45.4 | 63.4 | 63.4 | 190 | 190 | Score |
| י ערי | 16.2 | 16.2 | 16.2 | 16.2 | 16.2 | 16.3 | 16.3 | 16.4 | 16.6 | 17.4 | 19.5 | 19.5 | 23.9 | 23.9 | 33.4 | 33.4 | 100.0 | 100.0 | Query Match |
| 74933 | 53795 | 52661 | 52661 | 52661 | 52661 | 110000 | 5834 | 2000 | 1185 | 2701 | 199 | 187 | 201 | 189 | 200 | 188 | 202 | 190 | Query Match Length |
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| 7071075 | ADZ12703 | ADM74471 | ADC85355 | ADB72614 | ADA02876 | AEA61095_0 | ADC30699 | ABZ16307 | ACL27326 | AAD11619 | AAL50545 | ABZ80708 | AAL50546 | ABZ80709 | AAL50547 | ABZ80710 | AAL50549 | ABZ80712 | ID |
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| Abt 10752 Human bro | Adz12703 Hur | Adm74471 Human | Adc85355 Mouse | Adb72614 Human DP | Ada02876 Human DPT | Aea61095 Human LOC | Adc30699 Human nov | Abz16307 Arabidops | Acl27326 Rice abio | Aad11619 Mou | Aalsos45 Him | Abz80708 Hime | Aal50546 Dro | Abz80709 Droi | Aal50547 Crio | Abz80710 Cric | Aal50549 Black | Abz80712 Black | Description |
| , | Human can | nan car | use Dpt | nan DPT | in DPT | nan Loc | nan nov | pidops | ce abio | Mouse ooc | Himetobi | Himetobi | Drosophil | Drosophil | Cricket p | Cricket p | ck que | ck que | ; ; ; ; |

The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

a range of

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

Claim 1; Page 34; 39pp; Japanese.

Nakashima N,

Shibuya N,

Nishikawa S;

WPI; 2003-403230/38.

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| Adg97674 Mouse can Aax86847 P. squamu Adb51547 Primary r Adv40339 Rat cardi | Ada71938 Rice gene Aav17876 Cloned to Adr20357 Recombina Adr21486 Xenorhabd | Continuation (12 o Continuation (4 of Adr64012 Cotton cD | Adv87741 Streptoco Adv78994 Streptoco Continuation (4 of Continuation (11 o | | Abl12300 Drosophil Adk98945 S agalact Adk98938 S agalact Adk98941 S agalact Adk98940 S agalact |

ALIGNMENTS

RESULT 1
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PT Pseudoknot; secondary structure; cell-free protein synthesis; wheatgerm; albumen; impurity; higher-order structure; intergenic region; IGR-IRES; internal ribosome entry site; ss. 08-OCT-2002; 2002WO-JP010447. Black queen-cell virus. Black queen-cell virus derived pseudoknot sequence. ABZ80712 standard; RNA; 190 BP 17-OCT-2001; 2001JP-00319923. 24-APR-2003. WO2003033719-A1. 15-OCT-2003 ABZ80712; (NAAG-) NAT INST AGROBIOLOGICAL SCI. (WAKE-) WAKENYAKU KK. (first entry)

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RESULT 2
AAL50549
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Best Local Sim
Matches 190;
              have a higher-order structure that sustains translational activity-
promoting function. The RNA sequences of the invention are useful in the
synthesis of proteins and polypeptides for application in developing and
producing drugs. The RNA sequences of the invention are also useful in
                                                                                                                                                                                                                                                      Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                Claim 1; Fig 1-2; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CrPV-like virus; drug production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Black queen-cell virus RNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-2001; 2001JP-00016746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200261080-A1
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                                                                                                                              invention comprises seven RNA sequences (CrPV-like viruses)
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(first entry)
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translational activity-promoting function;
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The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Cricket paralysis virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in
                                                                                                                                                                                                                                                                                          Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translactivity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                    Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudoknot; secondary structure; cell-free albumen; impurity; higher-order structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2001; 2001JP-00319923
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Best Local
                                                The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Cricket paralysis virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cricket paralysis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CrPV-like virus; 88; higher-order structure; drug development; drug production; translational activity-promoting function;
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                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakashima
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                                                                                                                                                                                                                                                                                                                                                                                       synthesis of
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                                                                                                                                                                                                                                                                                                                                                                                    species
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Query Match Best Local Similarity

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Score 45.4; DB 8; Pred. No. 4.4e-05;

Sequence

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Best Local (
                                                                               The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                                                                                                       Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           albumen; impurity; higher-order structure; internal ribosome entry site; ss.
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 32; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakashima N,
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Pred. No. 3.5e
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intergenic region; IGR-IRES;
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RESULT 6
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XX Dros
XX CrPV
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                                                                                                                                  The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing an producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Drosophila C virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for applications.
                                                                                                          Sequence
                                                                                                                                                                                                                                                                       Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001; 2001JP-00016746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2001; 2001WO-JP000641
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RESULT 7
ABZ80708
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                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translactivity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page
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                                                                                                                                                                                                                                                                                                                                                Sequence 199 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Himetobi P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakashima N,
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   62
                                                         64
                                                                                                                  N
                                             AUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCU 123
                                                                                                                                                                  ACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUGCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAU--GGGGUGCAGCGUUCC. 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UUUACCU
   ACAUUUUUJAAGACCCUUAGUUAUUUJAGCUUUJACCGCCCAGGAU--GGGGUGCAGCGUUCC 119
                                                                                                                  AAAAUGUGUGAUCUGAUUAGAAGUAAGAAAUUCCUAGUUAUAUAUUUUUUAAUACUGCU
                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                60 A; 33 C; 40 G; 0 T; 66 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structural analysis
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                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                            Score 37; I
Pred. No. 0.
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                    85;
                                                                                                                                                                                                                                                                                    Length 199;
                                                                                                                                                                                                                                    Indels
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2376

AACAAUGUGAUCUUGCUUGCGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGC 62

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Matches
                          Query Match
                                                                           The present sequence is mouse occyte protein 8 (MOP8) cDNA. The present invention relates to egg specific surface proteins (antigens) and nucleic acids encoding them. The proteins of the invention are involved in egg-sperm binding and fusion. They are useful as immunogens in vaccine preparation for modulating fertility. In particular, the proteins are useful for producing antibodies which are useful for temporary, reversible contraception methods. The contraceptive vaccine is especially important livestock, e.g. cattle or pig. The invention also relates to the use of antibodies against such antigens for active immunisation or sterilisation of female animals
                                                                                                                                                                                                                                                                         New egg-specific surface proteins, useful as immunogens in preparation for modulating fertility, particularly useful t antibodies for temporary, reversible contraception methods.
                                                                                                                                                                                                                                                                                                                                                                            Herr JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-2001; 2001WO-US001718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse oocyte protein 8 (MOP8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD11619
                                                     Sequence 2701 BP; 754 A; 598 C; 631 G;
                                                                                                                                                                                                                                                 Claim 4; Page 35-37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VIRGINIA PATENT FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JAN-2000; 2000US-0177123P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
              Local
                                                                                                                                                                                                                                                                                                                                                2001-465367/50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 2701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UUUCACU 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UGCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUAGUGGACUUUAGGCUAAAGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yte protein 8; MOP8; egg specific surface protein; immunogen; fertility; contraceptive; active immunisation; sterilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uuuaccu
                                                                                                                                                                                                                                                                                                                                                                            Coonrod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Mouse oocyte protein 8 (MOP8)"
                                                                                                                                                                                                                                                                                                                                                                            SA,
             17.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1905
                                                                                                                                                                                                                                                                                                                                                                            Wright P;
Score 33; DB Pred. No. 1.8; 29; Mismatches
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                                                     704 T;
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 98;
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                          Length 2701;
                                                        14 Other
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 Gaps
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RESULT 10
ACL27326/c
ID ACL27336/c
ID ACL273
XX ACL273
XX ACL273
XX Be; ab
KW 88; ab
KW 88; ab
KW agricu
XX Oryza
PN WO2003
XX 21-JUN
PR 24-AUG
PR 26-SEP
PR 21-NOV
XX 21-JUN
PR 26-SEP
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PR 26-SEP
PR 26-SEP
PR 26-SEP
PR 26-SEP
PR 21-JUN
XX C1-JUN
XX 
                                                                                                                                                                                                                     The invention relates to novel abiotic stress responsive polynucleotides cand polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the cresponsiveness of a plant to abiotic stress. The invention is useful in egriculture. The nucleic acid is useful for determining whether a test color than been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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        Query Match
Best Local S
Matches 54
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24-AUG-2001;
26-SEP-2001;
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kreps J,
Moughamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-248011/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2002; 2002WO-US019668
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            54;
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                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNGENTA PARTICIPATIONS
                                                                                                                                                             1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1282; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITGATGATCAAGGAGTTGTGCTCTAGCTTTAGGGTCCCCTGAGGTATCTGAAGAACATA 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGGCTTTGGTCTCAATCACTACATTCATTTTAACCACATGGATGTTTGGACAGGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ИАИСААИАИСИАGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        папиениевалисассинский применений примен
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T, Provart
            Conservative
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; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
                                                                                                                                                     BP; 366 A; 319 C; 197 G; 303 T; 0
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                                    16.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cooper B,
N, Ricke
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        28;
    Score 31.6; D
Pred. No. 4;
28; Mismatches
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D, Zhu T;
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                                                                            Length 1185;
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GTTCTCAGATCAGTGTATAGCAGCTCTTTAGGTTACCAAAAGACCTGTAGTATCCAGAAA 1916

Query Match Best Local S Matches 37

Local Similarity

16.4%; 44.0%;

37;

Conservative

14;

33; 6;

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Gaps

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156

Score 31.2; DB Pred. No. 6.6; 14; Mismatches

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Length 2000; Indels

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                                                    The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000; 2000US-0227866P
26-JAN-2001; 2001US-0264647P
22-JUN-2001; 2001US-0300111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 144; SEQ ID NO 4112; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harper JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2001; 2001WO-US026685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2003
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10-APR-2003

24-SEP-2002; 2002WO-US030474

24-SEP-2001; 2001US-0324631P

Tang TY, Zhou P, Haley-Vicente D, Zhang J, Ghosh M, Drmanac RT; Ren F, Wang D, Xue AJ, Ma Y, / , Zhao QA, Asundi V, Wang Wang J, Wang Z, Wehrman T; Weng G;

2003-371981/35.

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or

Claim 1; SEQ ID NO 781; 1185pp; English.

The invention relates to 971 novel human cDNA sequences (ADC29919-CC ADC20889) and the polypeptides they encode (ADC30890-ADC31860). The cinvention also relates to nucleic acid sequences over 99% identical with CC the novel human cDNAs. The invention additionally encompasses expression CC vectors and host cells comprising a nucleic acid of the invention; the crecimpost production of a polypeptide of the invention; the compise of the invention; an antibody CC against a polypeptide of the invention; and methods of polypucleotides of polypeptide of the invention. The cinvention further discloses methods of peventing, treating or ameliorating a medical condition, kits comprising polynucleotide probes convention; methods for the identification of compounds that modulate the contig sequences corresponding to the convention and the polypucleotide and/or monoclonal antibodies for carrying out the methods of the contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32627) and the polypucleotide and/or polypeptide; and 767 CC contig sequences corresponding to the cDNA sequences of the invention are cuseful in diagnostics, drug screening, forensics, gene mapping, in the cartie, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are contigers and other neurodegenerative diseases, Alzheimer's diseases, Alzheimer's diseases, Alzheimer's alternary and an another and an anoth

The invention relates to a method (M1) for identifying one nucleic acid sequences useful as a biomarker for a disease detected. (M1) involves identifying nucleic acid sequences

e or more e to be comprising

Claim 11; SEQ ID NO 5; 27pp; English.

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RESULT 13

RESULT 13

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WP Sequence split into

WP Sequence split into

WP ARA61095_0

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WP ARA61095_2

WP ARA61095;

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                                                                                                                                                                      Identifying nucleic acid sequences as biomarker for disease, by identifying nucleic acid sequences comprising methylated CpG site and down-regulated in diseased cells and comparing its expression level with demethylated nucleic acid.
                                                                                                                                                                                                                                                                                                            GENBANK; BF589529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER CORP.
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RESULT 14
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CC regulated in diseased cells, comparing expression level of nucleic acid
CC sequences with that of demethylated nucleic acid sequences and
CC identifying nucleic acid sequences exhibiting increase in expression
CC after demethylation. Also described: (1) detecting (M2) the presence or
CC stage of a disease in a subject, which involves determining the degree of
CC methylation of one or more CpG sites on nucleic acid sequences in a
CC biological sample obtained from the subject, and determining the presence
CC of, predisposition to, or stage of the disease in the subject based on
CC tredegree of methylation; (2) monitoring the onset, progression, or
CC regression of a disease in a subject; and (4) a kit (1)
CC useful for diagnosis, prognosis, staging, monitoring, and therapeutic
CC treatment of a disease. (M1) is useful for identifying one or more
CC nucleic acid sequences useful as a biomarker for a disease to be
CC detected, where the nucleic acid sequences are useful for detecting, the
presence or stage of a disease such as cancer e.g. colorectal cancer in a
CC subject. The present sequence represents a specifically claimed human
CC genomic sequence for use in the method of the invention. Note - The
CC sequence data for this patent is not represented in the printed
CC specification but was obtained in electronic format from the USPTO web
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Best Local
                                                                                                                             New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                  WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2002; 2002WO-US041414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DPT carcinoma associated gene, SEQ ID NO:1394.
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Claim 1; SEQ ID NO 1394; 245pp; English

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                       02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                        Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DPT gene.
                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2001; 2001WO-US051291.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB72614 standard; DNA; 52661 BP
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                                                                                                             (SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
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                                        Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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31.2%; Pred. No. 29;
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Search completed: December 22, 2005, 08:40:40 Job time: 277.574 secs
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.2%; Score 30.8; DB 10; Length! Best Local Similarity 31.2%; Pred. No. 29; Matches 43; Conservative 28; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 442; 2304pp; English.
                                                                                             149 UGUUUAGAAGAUUAGGUA 166
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8616 GGTTCACAAGGTAATGTA 8599
                                                                                                                                                                                          B676 AGGTTTTTGTGTGAACAAATTTTTATTTCATTTGGGTCAATACCTAGGAGTGAGATTGCT 8617
                                                                                                                                                                                                                                                                                     8736 ATATTTTATATGAATTACATAAATGTAATTATAAAGTTGATATAAACATCTATGTAT 8677
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
          Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-088-750C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        December 22, 2005, 07:31:33 ; Search time 1988.22 Seconds (without alignments) 4471.109 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41078325 seqs, 23393541228 residues
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Copyright (c) 1993 - 2005 Compugen Ltd.
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9b_est7::*
9b_9s81::*
9b_9s82::*
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gb_est2:*
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CO153155 EN01401.5
CO153454 EN02010.5
CO153454 EN02756.5
CO153765 EN02756.5
CO337794 EN15317.5
CC0248993 SCSBFLL10
CW675417 OP BA007
BQ441285 AGENCOURT
CK312556 SB02035A1
BX120183 Danio rer
BG499554 602546703
AJ562935 Cryptcspo
BX615168 BX615168
CL685543 FRI0141C
R25253 yh41h12.r1
AQ680797 HS 5488.A
CZ858355 OC BA025
CZ958530 308752 TO
ALIO1451 Drosophil
CW108676 104 480 1
CZ042704 OM BA002
CW328338 104_824_1
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | <u>υ</u> | 34 | ω U | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 |
| 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32.2 | 32.2 | 32.2 | 32.4 | 32.4 | 32.4 | 32.4 | 32.4 | 32.6 | 32.6 | • | 32.8 | • | 32.8 | 32.8 | 32.8 |
| 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.8 | 16.9 | 16.9 | 16.9 | 17.1 | 17.1 | 17.1 | 17.1 | 17.1 | 17.2 | 17.2 | 17.2 | 17.3 | 17.3 | 17.3 | 17.3 | 17.3 |
| 849 | 842 | 807 | 754 | 716 | 712 | 522 | 727 | 719 | 899 | 899 | 883 | 723 | 579 | 514 | 822 | 759 | 451 | 977 | 781 | 767 | 763 | 724 |
| æ | œ | 7 | œ | σı | 7 | Ŋ | ш | 9 | 10 | 10 | 7 | 10 | N | N | 10 | 10 | σ | 9 | 10 | 10 | N | 10 |
| DN087727 | DR860385 | CK312357 | DN035261 | BQ781365 | CK308262 | BY471748 | AV707635 | CE167648 | CZ057824 | DU074448 | CO116428 | CZ754700 | BG080560 | BB703319 | BX221224 | BX207527 | CA433304 | CC217149 | CW375429 | CW359111 | BE569614 | CL381173 |
| DN087727 JGI_CABE1 | DR860385 JGI_CABG4 | CK312357 SB02011A2 | | BQ781365 UI-R-FF0- | CK308262 SB02046A1 | BY471748 BY471748 | AV707635 AV707635 | CE167648 tigr-gss- | CZ057824 OM_Ba005 | DU074448 69473 Tom | CO116428 GR_Eb018 | CZ754700 OCBa010 | BG080560 H3055A10- | BB703319 BB703319 | BX221224 Danio rer | BX207527 Danio rer | CA433304 UI-H-CO0- | CC217149 CH261-23E | CW375429 fsbb001f0 | CW359111 fsbb001f0 | BE569614 601328256 | |

ALIGNMENTS

| COLS3155 COLS3151 COLS3155 COLS3151 COLS3155 COLS3155 COLS3151 COLS3155 COLS3151 COLS3155 COLS3151 COLS3155 COLS3151 COLS3151 COLS3155 COLS316 COL | | | | | | | |
|--|---|--|---|--------------------|---|--|---|
| ### A33 bp mRNA linear ine Exelixis FlyTag MNO8 BlueScript Droso r cDNA clone EN01401 5, mRNA sequence. GI:48907156 melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) melanogaster (fruit fly) prosophilidae; Drosophila. (a | | Query Mato Best Local Matches | ORIGIN | FEATURES source | AUTHORS TITLE JOURNAL COMMENT | KEYWORDS SOURCE ORGANISM REFERENCE | RESULT 1 CO153155 LOCUS DEFINITION ACCESSION VERSION |
| | AUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUAGUGCUAUU : : : : : : : : : : : : : | 24.7%; Score 47; DB 7; Length 433; 37.7%; Pred. No. 0.0008; vative 42; Mismatches 70; Indels 2; Gaps | /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="mRNA" /db_xref="taxon:7227" /clone="EN01401" /cell line="mbn2" /clone_lib="Exelixis FlyTag MN08 BlueScript" /note="Vector: pBluescript; Site 1: Notl; Site 2: XhoI; oligodT primed from LPS induced mbn2 cell line." | 9472 EST, | Nakanishi,M., Muzong,C., Peterson,E., Laufer,A., Leung,W., Platt,D. and Swimmer,C. Exelixis FlyTag EST Project MNO8 Library Unpublished (2004) Contact: Stapleton, M. | EST. Drosophila melanogaster (fruit fly) Drosophila melanogaster Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 433) | 433 bp mRNA linear 401.5prime Exelixis FlyTag MN08 BlueScript Droso nogaster cDNA clone EN01401 5, mRNA sequence. 3155 3155.1 GI:48907156 |

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RESULT 2
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Best Local Similarity
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; In
Neoptera; Endopterygota; Diptera; Brachycera
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 486)
Nakanishi, M., Muzong, C., Peterson, E., Laufer
and Swimmer, C.
                                           249
                                                                                                                                                                                   130 TTAATAATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCTAT-TGGCAGCCCCATA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One Cyclotron Rd, Berkeley, CA 94720
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST,
Plate: EN.20 row: A column: 10
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Location/Qualifiers
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                                           AAC
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                                                                                                              ATATCCAGGACACCCTCTCTGCTTCTTATATGATTAGGTTGTCATTTAGAATAAGAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       oligodT primed
                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site 1: NotI; Site
oligodT primed from LPS induced mbn2 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
|/mal_type="mRNA"
|/db_xref="mEAXON:7227"
|/clone="EN02010"
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                                                                                                                                                                                                                                                                                                                              Score 47; DB Pred. No. 0.000
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tches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                Length 486
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Muscomorpha;
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CO153765
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 539)
                                                                                                                                             melanogaster cDNA clone CO337794
                                                                                                                                                            EN15317.5prime Exelixis FlyTag MN08 BlueScript Drosophila melanogaster cDNA clone EN15317 5, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 490)
Nakanishi, Muzong, C., Peterson, E., Laufer, A., Leung, W., Pl
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One Cyclotron Rd, Berkeley, CA 9472
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST,
Plate: EN.27 row: E column: 8
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CO153765
CO153765.1 GI:48907766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGTGATCTTGCTTCCTTATAC-AATTTTGAGAGGTTAATAAGAAGGAAGTAGTGCTATT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                           287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Exelixis FlyTag MN08 BlueScript"
/note="Vector: pBluescript; Site_1: NotI; Site_2:
oligodT primed from LPS induced mbn2 cell line."
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|mal_type="mdNA"
|db_xref="taxon:7227"
|clone="EN02756"
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                                                                                                                           GI:49398069
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Pred. No. 0.00082;
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3 BlueScript Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
                                                                        Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                             Vettore, A.L., da Silva, F.R., Korne libraries that made SUCEST Genet Mol Biol 24 (1-4), 1-
                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Saccharum; Saccharum officinarum
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3', mRNA sequence.
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One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATCCAGGACACCCTCTCTGCTTCTTATATGATTAGGTTGTCATTTAGAATAAGAAAAT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTGATCTTGCTTCCTTATAC-AATTTTGAGAGGTTAATAAGAAGGAAGTAGTGCTATT 148
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/note="Vector: pBluescript; Site_1: NotI; Site_2: XhoI;
oligodT primed from LPS induced mbn2 cell line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Drosophila melanogaster"
|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Score 47; DB 7;
37.7%; Pred. No. 0.00083;
tive 42; Mismatches 70
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marum officinarum cDNA clone
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                  information can be found Center (BCCC) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 539;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472 AAAGATTTGATGTGACGAGACATCTGAAAATTTTTGGTAAAATTTTTGGTATCTAAACGGT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 CAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAU 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 GUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUC
                                                                                                                                                                                                                                                                                               SanMiguel, P., Westerman, R., Kim, H., Stum, D., Rao, K., Luo, M., Jetty, R., F. Hatfield, J., Soderlund, C., Wing, R. & OMAP Project - Purdue University
                                                                                                                                                                                                                                                                                                                                                                                                 Oryza punctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                             Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s. Bases 36-861 of the raw sequence (length 1079) were retained after
                                                                                                                                                                                                                                       Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OP_Ba0075D07.f OP
                                                          clipping
                                                                                                                                                              Tel: 7654963621
Fax: 7654967255
                                                                                                                                                                                               Purdue University
915 W. State St.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza punctata
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  FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
                                         PCR PRimers
                                                                                                                                         Email: sjackson@purdue.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCTAGTTTCTCTAC 397
                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 826)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.4%; Score 36.8; D; 30.1%; Pred. No. 1.5; tive 33; Mismatches
                                                                                                                                                                                                 West Lafayette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _Ba Oryza
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punctata genomic clone OP_Ba0075no7
                                                                                                                                                                                                   IN 47907,
                                                                                                                                                                                                                                                                                                                    Yu,Y., Wissotski,M., Yost,D., Kudrna,D., Muller,C., and Jackson,S.A.
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Plate: 105 row: E column: 02
Seq primer: SP6 Promoter primer.
                                                                                                                                         /note="Torgan: Inflorescence at begining of development (1cm long); Vector: pSport1; Site_1: Sal1; Site_2: NotI; An unidirectional cDNA library generated from [Inflorescence at begining of development (1cm long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-28 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
                                                                                                              http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharum officinarum"
/mol_type="mRNA"
/db xref="taxon:4547"
/clone="SCSBFL1105E02"
DB 6;
Length 714;
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62;

Indels

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Gaps

100 0

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AACATTGAATATTTTGATAATATGTTTGÄTTTTGGTTTGAAAAATACTAATATATTTTTC 97
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Plate:
                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCR2345 row: c column: 07 High quality sequence stop: 486. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 831)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ441285.1 GI:21180361
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATAAACTTGATAAAACTTAGAGAAGTTTGACTAGAAAAAAAGTCAAACGACTTA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUC 132
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0075 row: 1
/db_xref="taxon:9606"
/clone="IMAGE:6105534"
/clone="IMAGE:6105534"
/clone="IMAGE:6105534"
/clone="DH10B (T1 phage-resistant)"
/clone="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccgcctcggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCCC-3' and 3' adaptor sequence:
                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Young leaves"
/lab_host="DH1OB-T1 phage resistant"
/clone_llb="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
/clone="OP__Ba0075D07"
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Euarchontoglires; Primates;
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Pred. No. 3.3;
34; Mismatches
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 ACAGCATGATGTTCCCATGGTAGTTÄGAATTCTTACÄTGGTÄCÄGGCTTCTÄGGÄGGCAC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AUCAAUAUCU 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 AUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCU 123
                                                                                                                                                                                                                                                                                                                          Vector Trimming: Cross match from Washington University Genome Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script. This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      751 bp mRNA linear EST 01-MAI
SB02035A1H11.fl normalized Keck-Tagu Library SB02 Taeniopygia
guttata cDNA clone SB02035A1H11.fl 5, mRNA sequence.
CK312556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50,
                                                                                                                                                             Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 751.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior Unpublished (2004)
Contact: David F. Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 751)
Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M., Clayton, D.F., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
                                                                                                                                                                                                                                 Insert Length: 751
Plate: SB02035A1 r
                                                                                                                                                                                                                                                                              FORWARD: TAATACGACTCACTATAGGG (T7)
BACKWARD: ATTAACCCTCACTAAAG (T3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dclayton@uiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B107 CLSL, 601 S.
Tel: 217 244 3668
Fax: 217 244 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Illinois
B107 CLSL, 601 S. Goodwin, Urbana, IL 61801,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taeniopygia guttata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAGTGGAAGCTACAGGTCTTTAAGGTCTACCTTGGAAAAGGGGTGGGCAGGATCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ם, שנת
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
/clone="SB02035A1H11.f1"
/tissue_type="brain"
/dev_stage="late embryo,
                                                                    organism="Taeniopygia/mol_type="mRNA"
/db_xref="taxon:59729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.7%;
                                                                                                                                                                                                           s1 Std Error: 0.00
  row: H column: 11
cGACTCACTATAGGG (T7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 35.6; I
; Pred. No. 3.8;
21; Mismatches
  embryo, post-hatch days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 01-MAR-2004
  10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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  45
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linear

EST 27-MAR-2001

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Local Similarity
                                                                              63 UAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 608)

1 (bases 1 to 608)

1 humbray, S. J., Huckle, B. and Durham, J. L.

Direct Submission

Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of part of the Daniokey BAC Library created by R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCAACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAAUCUGCAAGUAGU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX120183.1 GI:27951099
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio genomic clone
BX120183
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keygene. Further details:
                           TTTAGGATGAATATTTTTACATGTTTAAAATTTAACATACAAG
                                                                                                                                                                                     AACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTATTCCTTTCTACTCCAACTGTGTAATGAATAGAACTTCATTTTCTCCTTA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGAAGCTGATCAAGATGGAGATAGTGCCATCTCCTTTGCAGAATTTGTAAAGGTTTT 591
                                                                                                                                                                                                                                          18.3%;
ilarity 34.3%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and adult (pooled)"

/lab_host="PH10B"

/clone_lib="normalized Keck-Tagu Library SB02"

/clone_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: pBS II SK(+); Site_1:

/corr[(5' side of insert); Site_2: NotI (3' side_of
insert); The library was constructed and normalized as
described by Bonaldo, M.F., Lennon, G. and Soares, M.B.
(1996), Genome Research 6(9): 791-806. An identiying tag
was added at the 3'during cDNA synthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Danio rerio"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:7955"
/clone="DKEY-69K2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.6%;
                                                                                                                                                                                                                                       ; Score 34.8; DI
; Pred. No. 6.4;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 35.4; Di
; Pred. No. 4.3;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 bp DNA linear
DKEY-69K2, genomic survey
                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7;
                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                         Length
                              156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC 69K2. 69K2 is Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 13-MAR-2003
                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                           CPA562935
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
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BG499554
LOCUS
                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
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     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                544 CAATCTAGGTTTGCGTCTATGGATGGTTGAATGTTCGTTGGTGTCAGAGCGGAACATGATT
                                                                                                                                                                                                                                                                                                                                                                             484 GGTAACAAAGTTCTATCGGTGTATGACATGAAGGGGGTGCGTCTAGGGAAATCAACAAAT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                  23
CPA562935 601 bp DNA linear (Cryptosporidium parvum GSS, PAC clone pica_0012_e08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1480 row: e column: 02
High quality sequence stop: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1228)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602546703F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG499554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG499554.1 GI:13461071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domo sapiens (human)
                                                                                                                                                              GGGTTAAGTATAGGTGGTAACAAAGTAACTATCAGGAA
                                                                                                                                                                                                                 GUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAA 180
                                                                                                                                                                                                                                                                                                                     CUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCCUAUCAAUAUCUAGGAGAACU 142
                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUAC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Torgan: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgcctcggcc); Site 2: SfiI (ggccgcctcggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCCGACATG-dT(30)BN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH_MGC_60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:4669033"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.3%; Score 34.8; DE 35.4%; Pred. No. 7.3; tive 25; Mismatches
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REFERENCE AUTHORS

TITLE JOURNAL

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GSS 11-AUG-2003 T7 end

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603

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Matches Query Match

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                                                                                                                                                                                                                                                                                           BP912007 Adiantum capillus-veneris prothallium Adiantum capillus-veneris prothallium Adiantum capillus-veneris cDNA clone YMU001_000012_A01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
capillus-veneris
J. Plant Res. (2005) In press
Contact: Daiguke Yamauchi
                                                                                                                                                         BP912007.1 GI:67218050
EST.
Adiantum capillus-veneris
Adiantum capillus-veneris
Adiantum capillus-veneris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Filicales; Pteridaceae;
Moniliformopses; Filicophyta; Filicopsida; Filicales; Pteridaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAY-2003) Dear P.H., PNAC Biotech Division,
Laboratory of Molecular Biology, Hills Road, Cambridge, Co
2QH, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bankier, A.T., Spriggs, H.F., Fartmann, B., Konfortov, B.A., Madera, M., Vogel, C., Teichmann, S.A., Ivens, A. and Dear, P.H. Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum Genome Res. 13 (8), 1787-1799 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence, genomic survey sequence.
AJ562935
AJ562935.1 GI:31337755
GSS; genome survey sequence.
                                                        Fukuda, H. and Wada, M. Analysis of Expressed
                                                                                                Yamauchi, D., Sutoh, K., Kanegae, H., Horiguchi, T., Matsuoka, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTATTTGAAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTCTGAATATGAAGGCCATAAGCTAGAGTTAAGATATTCTTAGTTTTGATATCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="pica_0012_e08"
/clone_lib="pica"
/dev_stage="oocyst"
/note="T7 end sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/serotype="Type 2"
/isolate="Iowa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:5807"
'chromosome="0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Cryptosporidium parvum"
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29.5%;
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                                                          Sequence Tags in Prothallia of Adiantum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.4; DB 11;
Pred. No. 8.5;
2; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GCAGCCCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 GTATAGCTÁCACCTCGTGTGCCTACCTGTÁTGTTTGTTTTGCGCACATAGGCCCCTTGTGTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX615168 Normalized Anopheles Head (NAH) CDNA Clone AGAD347TR, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                               Center for Tropical Disease Research and Training University of Notre Dame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryg
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anopheliae; Anopheles
1 (bases 1 to 700)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX615168
                                                                                                                                                                                                                                                                                                              Email: frank.h.collins.75@nd.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H. Anopheles gambiae EST, Center for Tropical Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dyamauch@sci.u-hyogo.ac.
This clone was obtained at our
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Tel: 574-631-9245
Fax: 574-631-3996
                                                                                                                                                                                                                                                                                                                                                                                              Notre Dame, IN 46556,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-792-67-4920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2167 Shosha, Himeji, 671-2201, Japan
Tel: 81-792-67-4939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frank H.
/lab_host="E. coli DH10B"
/clone lib="Normalized Anopheles Head (NAH) Library"
/clone lib="Normalized Anopheles Head (NAH) Library"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR1 (5'end); Site_2: Not1 (3'end); a
directionally cloned and normalized, oligo-T primed cDNA
library constructed from strain 4arr adult mosquito heads.
Equal numbers of sugar fed males, sugar fed females and 6,
24 and 48 hr post blood meal females were used: Bonaldo,
Lennon & Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
                                                                                                                                                                                                          /db_xref="taxon:7165"
/clone="AGAD347TR"
                                                                                                                                                                                                                                                   organism="Anopheles gambiae"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="YMU001_000012_A01"
/tissue_type="prothallium"
/clone_Tib="Adiantum capillus-veneris prothallium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:13818"
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our laboratory.
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Library Anopheles
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                                                                                                            42 UAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Srinivasan,J., Otto,G.W., Kahlow,U., Geisle
AppaDB: an AcedB database for the nematode
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazas, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CL685543.1 GI:50193876
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CL685543 902 bp DNA linear GSS 09-JUL-20
PRI0141c_B08_2 - PRI0141c.BR (902) Mixed stage fosmid library of pacificus var. California Pristionchus pacificus genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer:
Class: fosmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAATCTAACTGGTGCTATTTTTTATATCGCACCTGTTTTGAGGTATTATGCTGAATCAT 578
                                 AAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUU 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTGAAAAAAGTCCCATCAATATGTTGAAGTAATGTGCT 619
ACTATTCGTCAACTGCAATTCATTCGATAAATTTTTGGAAATATGCTATTTTAAGATTATA 872
                                                                         TTTATACTGTGCAAGTACTTCTCCAATTTGAGTGAGCGTCGATTCGGAGATTCGGAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 902)
nivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
wDB: an AcedB database for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 00497071601498
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                                                                                                                                                                                                                                                                                                                       organism="Pristionchus
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                               /clone_lib="Mixed stage fosmid library of P. pacificus
ar. California"
                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                                                               note="Vector:
                                                                                                                                                                                                                                                                                                     db_xref="taxon:54126"
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Pred. No. 14
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Pred. No. 19;
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Matches Best Local

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Conservative

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Similarity

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AUTHORS
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ORGANISM
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R25253/c
LOCUS
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                                                         ORIGIN
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               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stops: 285
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1608 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 402)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R25253 402 bp mRNA linear EST 24-APR-yh41h12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:132359 5' similar to SP:S35755 S35755 SIAH-2 PROTEIN - ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Insert Size: 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R25253.1 GI:781388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 285.
                                                                                   /mol_type="max.../db_xref="GDB:537954"
/db_xref="taxon:9606"
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                                                                         constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                          sex="Female"
                                                                                                                                                                                                                                                                                                                          clone="IMAGE:132359"
17.5%; Score 33.2; 32.8%; Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louis,
                 Length 402;
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                                                                                                                                                                                           primer [5'
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Db 74 GACTTTCGTAAACTTATTTGGGCATAGTGCTCTATGTTTAATAAAGGTTTTT 15

Qy 169 CUCUAAACAGAACA 182

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Db 14 ATAGAAAAAAAA 1

Search completed: December 22, 2005, 15:21:08

Job time: 1991.51 secs

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Result
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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

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  GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd
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Sequence 3, Appli
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Sequence 108154, A
Sequence 1724, A
Sequence 1736, A
Sequence 17124, A
Sequence 5118, Ap
Sequence 20800, A
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| SULT 2 3-09-270. Sequence Patent N GENERAL APPLICA TITLE C | | | | | Query M Best Lo Matches | RESULT 1 US-09-270-767- Sequence 107 Patent No. 6 GENERAL INFO APPLICANT: TITLE OF IN. FILE REFERE CURRENT APP CURRENT APP CURRENT PIL NUMBER OF SIL NUMBER | | 044444 001364 001364 | 33333 0876 | . W W I | 330 310 310 | 226 |
| -767-1 1635 NO. 67 INFOR INFOR SFEREN | 187 AC 701 AA | 127 A | 67 GI 582 T | 7 AI - 523 A' | atch cal S 69 | 767 | | 222222 8888 | 2222 282 283 283 2444 | 222 | 22 22 22 28 28 28 28 28 28 28 28 28 28 28 28 28 2 | 2222 2888 6666 |
| 6354 (4, Appli (03491 MATION: Comburger TENTION: (CE: File | ACC 189 | AUAUCUA FATCCAG | UUGGAAU ; ; TAATAAT | UGUGAUCI : : : TGTGATC | imilarity ; Conserva | ppli 91 ION ION Fil DATE DATE TION DATE | | | . 4 4 4 | 944 | 5555 | 5555 |
| ication US/0927076 r et al. Nucleic acids and e Reference: 7326- | | ANDAUCUAGGAGAACUGUGCUAUGUUUDAGAAGAUUNGGGUAGUCUCUAAACAGAACAUUU | GUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUC : | AUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUU : : : :: :: :: : : : :: ATGTGATCTTGCTTCCTTATAC-AATTTTGAGAGGTTAATAAGAAGGAAGTAGTGCTATT | 24. 37. tive | cation r et al Nuclei e Refei nUMBER 18999 S: 62999 S: 6299 Cr. 2 | | 2070 2070 2070 2070 2070 2070 2402 | 39318 44499 70014 | 783 | 121234 140315 147840 | 601 1569 49526 108060 |
| US/ c ac | • | UGUG : : | ACTO HUCCUS | TTTP | 7*; | US/0 L. ac lc ac cence ?: US / US / US / US / US / US / US / US | | (J) (J) (J) (J) (J) (J) (J) (J) (J) (J) | | | | |
| 7092: 1d8 | | CUA | TTT | TAC | N1 | e 978 7 | _ | US-0 US-0 US-0 | | 1 1 | | US-0 US-0 US-0 |
| | | TICI | AGGU | -AAT | Score 47; Pred. No. ; Mismat | 70 B 0 | ALIGNMENTS | 8999999 | , 9 9 9 9 | 9 8 9 | 9999 | 9999 |
| 7 . prot. 094 | | UAGA : TATA | UUAC | ouug ::: TTTG | 47; No. matc | 7 d prote -094 0,767 | NMEN | 82-25 95-11 95-16 36-26 79-18 67-96 62-46 | 199-0 | 52-5 | 0-01 | 19-0 19-0 19-0 |
| teins | | AGAU : TGAT | GCUC : TGTT | CACA AGAG | DB 1.4e ches | teins | TS | 6-1 5-1 5-1 7-1 7B- | 16-1 16-1 16-1 | 69-1 | 16-1 16-1 16-1 | 16-4 52-3 16-1 |
| 69 O H | | TAGG | CAGO | GUAU - GTTA | 3; -05; 70 | ia O H | | | 3798 3798 2711 7110 | 15 | 4142 4141 5236 5779 | 2431 981 985 3159 |
| : Drosophila | | HUAGUCU : : HTTGTCA | AUCGGU : ATGCCT | JAAAAUCI ATAAGA | Length : | | | | | | | |
| phi l | | CUAA. | GGAU : AT-T | AGGA | 134 18 | phil: | | 8 8 8 8 8 8 | 9 9 9 9 | 0 0 0 | | 9 8 8 8 8 8 |
| a melanogast | | ACAGAA GAATAA | UAGCAGCCCUAUC : : TGGCAGCCCCATA | AGUAGU : : AGTAGT | 5; 2; | Drosophila melanogast | | Sequence Sequence Sequence Sequence Sequence Sequence | acuent acuent acuent acuent | quence | sequence sequence sequence | Sequence Sequence Sequence Sequence |
| nogas | | CAAUI - GAAAA | CCCA: | GCUAL : GCTA: | Gaps | nogas | | 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 11, Appl | 1379 1271 1711 | 15, | 141, 1523 1577 | 424: 3981 1298 1318 |
| ster | | 7 | 6 P | υ o | œ. | g te r | | Appl Appl Appl Appl Appl Appl Appl | 10, 10, 11, 12, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13 | App | 79, 11 | 31, A |
| | | 98 | 26 40 | 6 | 2 | | | | , ש פייי | , – – | P P P P | A D. G G |

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APPLICANT: Coontrod, Scott A
APPLICANT: Herr, John C
APPLICANT: Wright, Paul
TITLE OF INVENTION: Egg Specific Surface Proteins
FILE REFERENCE: 00498-07
CURRENT APPLICATION NUMBER: US/10/181,612
CURRENT APPLICATION NUMBER: US 60/177,123
PRIOR APPLICATION NUMBER: US 60/177,123
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 7
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16354
LENGTH: 1345
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Patent No. 6962988
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                                                                             NAME/KEY: misc feature
LOCATION: (2382)...(2382)
OTHER INFORMATION: "n" meaning
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LOCATION: (2366)...(2366)
OTHER_INFORMATION: "n" meaning
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LOCATION: (2337)..(2337)
OTHER_INFORMATION: "n" m
                                       NAME/KEY: misc feature LOCATION: (2447)..(2447)
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ORGANISM: Drosophila melanogaster
 NAME/KEY:
                          OTHER INFORMATION: "n"
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misc_feature
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RESULT 4
US-09-949-016-13430/c
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR TILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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NAME/KEY: misc_feature

100aTION: (2525)...(252
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LOCATION: (2666)...(2666)
OTHER INFORMATION: "n" m
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LOCATION: (2630)..(263
OTHER INFORMATION: "n"
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LOCATION: (2580)...(2580)
OTHER INFORMATION: "n" meaning
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LOCATION: (2509)...(2509)
OTHER INFORMATION: "n" meaning
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LOCATION: (2577)..(2577)
OTHER_INFORMATION: "n" meaning
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LOCATION: (2481)...(2481)
OTHER INFORMATION: "n" m
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OTHER INFORMATION: "n" m
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OTHER INFORMATION: "n" meaning
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US-09-949-016-13430
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRSESEQ for Windows Version 4.0
SEQ ID NO 13430
LENGTH: 87205
TYPE: DNA
Sequence 108154, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 16102
LENGTH: 36661
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16102, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                              ATATTTATATAATGAATTACATAAATGTAATTATAAAGTTGATATAAACATCTATGTAT 677
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                                                                                                                                          GGTTCACAAGGTAATGTA 599
                                                                                                                                                                               UGUUUAGAAGAUUAGGUA 166
                                                                                                                                                                                                                                                           AGGUUTUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCUAGGAGAACUGUGCUA 148
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                                                                                                                                                                                                                      AGGITITIGIGIGAACAAAITITTATITICATITIGGGTCAATACCTAGGAGTGAGATIGCT 617
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                                                                                                                                                                                                                                                                                                                                                                                                   16.2%; Score 30.8; Di 31.2%; Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                                                                                                 28; Mismatches
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ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(250352)
OTHER INFORMATION: n = A,T,C
US-09-949-016-14724
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; ORGANISM: Human
US-09-949-016-108154
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Best Local Similarity 35.4
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SEQ ID NO 14724
LENGTH: 250352
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                                                                                                                              Query Match
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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47624 GAACGCAAATTATGGAGACACTAAACAAGGAAAAAATTGCAAAATGATGATTAAGTGTAT 47683
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                       GGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUAC 82
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                                                                                      Conservative
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                                                                                                         15.8%; Score 30; DB 3; Length 250352; 35.4%; Pred. No. 25;
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MOLECULE TYPE: DNJ
HYPOTHETICAL: NO
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CLONE: W10 3'end
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LENGTH: 241 base pairs
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NAME: Poulos, Gail E.
REGISTRATION NUMBER: 36,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hanna, Wayne W.
APPLICANT: Roche, Dominique
TITLE OF INVENTION: Nucleic Acid Markers for
TITLE OF INVENTION: Apospory-Specific Genomic Region
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mes 38; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                        139 AACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAACAAUUU 186
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                                                                                                                                                                                                                                                                           GTĂCCAAATTATGTTGĂCAATTCAATTTCTAGAATTTTAGAGCACATTAATTATTAG
                                                                                                                           AATTATTATATCATGAGCATGAGATGTAAAATCGAATCATAAGAATTT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 4.2;
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; ORGANISM: Human
US-09-949-016-16936
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: VENTER, J.
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                                                                              Matches
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                 SEQ ID NO 17123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ
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                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(42954)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
FEATURE:
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30513 TAAAAAATTAGCCAGGCGTGGTATGTCTGTAGTCCCAGCTACTGGGGTGGTTGAGGCAGG 30572
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                              42 UAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCC 101
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Similarity 39.6%;
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nilarity 41.5%;
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Pred. No. 29
                                                                                                Score 29;
Pred. No.
                                                                              Mismatches
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                                                                                              DB 3;
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OF DETECTION AND USES THEREOF
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; LOCATION: (1)...(42954)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17124
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Patent No. 6703491
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17124
LENGTH: 42954
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5518
LENGTH: 353
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Best Local Similarity
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                                                                                                                                  Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                  TYPE: DNA
ORGANISM: Drosophila melanogaster
-09-270-767-5518
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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42 UAUAAAAUCUGCAAGUAGUGCUAUUGGUGGAAUCACCGUACCUAUUUAGGUUUACGCUCC 101
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                          AAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACCUAUUUA 89
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                                                                                      15.2%; Score 28.8; DB 3; ilarity 38.9%; Pred. No. 8.7; Conservative 17; Mismatches 27;
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                                                                                         27;
                                                                                                                                    Length 353;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

FILL OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

FITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

PRIOR PRIOR DATE: 2000-09-08
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; Sequence 43832, Application US/09949016
; Patent No. 6812339
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; ORGANISM: Drosophila melanogaster
US-09-270-767-20800
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US-09-949-016-43832
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20800
LENGTH: 353
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LENGTH: 601
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Best Local :
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34.0%; Pred. No. 10;
tive 23; Mismatches
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US-09-949-016-43877/c

US-09-949-016-43877/c

Sequence 43877, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR RILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR RILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 43877

LENGTH: 601

TYPE: DNA

ORGANISM: Human

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Search completed: December 22, 2005, 15:30:27 Job time: 82.9079 secs
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Best Local S
Matches 190
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Publication No. US20040166486A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: NAKASHIMA, Yasushi
ITILE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 202
TYPE: RNA
ORGANISM: Black Queen-Cell Virus
                                   181
181
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                   CAAUUUACCU 190
                                                                                             CCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAA
                                                                                                                                                                       GCUAUUGGUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGC
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CAAUUUACCU 190
                                                                       CCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAA
                                                                                                                                                                                                                                                                                                  100.0%; Score 190; DB 7; ilarity 100.0%; Pred. No. 2.1e-52; Conservative 0; Mismatches 0;
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RESULT

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FITTLE OF INVENTION: OCCUPANTS OF INVESTIGN IN INVESTIGN OF SECTION NUMBER: US/10/088,750B; CURRENT APPLICATION NUMBER: US/10/088,750B; CURRENT FILING DATE: 2002-03-20; PRIOR APPLICATION NUMBER: UP P2001-016746; PRIOR FILING DATE: 2001-01-25; PRIOR APPLICATION NUMBER: PCT/JP01/00641; PRIOR FILING DATE: 2001-01-31; NUMBER OF SEQ ID NOS: 12; SOFTWARE: PatentIn version 3.2; SEQ ID NO 3; LENGTH: 201
TYPE: RNA ORGANISM: Drosophila C Virus
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; ORGANISM: Cricket Paralysis Virus
US-10-088-750B-4
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                                              Matches 110;
                                                                   Query Match
Best Local (
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Best Local Similarity
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LENGTH: 200
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APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR APPLICATION DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CUAUCAAUAUCUAGGAGAAACUGUGCUAUGUUUAGAAGAUUAGGUAGUCUCUAAACAGAAC 181
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7 AUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUU
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                                              Conservative
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                                                                   23.9%;
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                                          Score 45.4; DB 7;
Pred. No. 0.00015;
0; Mismatches 71;
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Pred. No. 1.7e-10;
0; Mismatches 61;
                                                                                    Length 201;
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; LENCTH: 199
; TYPE: RNA
; ORGANISM: Himetobi P Virus
US-10-088-750B-2
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US-09-925-065A-611338/c
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                                                                                                                                                    Sequence 611338, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
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Best Local Similarity 53.5
Conservative
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 3190-015
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                124 АИСАЛИЛИСИЛЕСЬКА СИБИСИЛИСИИ ПОВЕТИТЕЛЬНЫ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCU 63
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                                                                                                                                                                                                                                                                                                                                                                                                         UGCAAUAUCCAGGGCACCUAGGUGCAGCCUUGUAGUUUUUAGUGGACUUUUAGGCUAAAGAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAUUUUUAAGACCCUUAGUUAUUUAGCUUUACCGCCCAGGAU--GGGGUGCAGCGUUCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAUGUGUGAUCUGAUUAGAAGUAAGAAAAUUCCUAGUUAUAAUAUUUUUAAUACUGCU
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Pred. No. 0.09;
0; Mismatches
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                                                                                          in the Human
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FILING DATE: 2000-10-24
APPLICATION NUMBER: US 60/252,147

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US-09-925-065A-611339/c
US-09-925-065A-611339/c
Sequence 611339, Application US/09925065A

| Publication No. US20050228172A9
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single
| TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
| PILE REPERENCE: 108827,135
| CURRENT APPLICATION NUMBER: US/09/925,065A
| CURRENT FILING DATE: 2001-08-08
| PRIOR APPLICATION NUMBER: US 60/243,096
| PRIOR APPLICATION NUMBER: US 60/252,147
| PRIOR APPLICATION NUMBER: US 60/252,147
| PRIOR APPLICATION NUMBER: US 60/252,092
| PRIOR APPLICATION NUMBER: US 60/250,092
| PRIOR PILING DATE: 2000-11-20
| PRIOR PILING DATE: 2001-01-16
| PRIOR APPLICATION NUMBER: US 60/251,766
| PRIOR APPLICATION NUMBER: US 60/261,766
| PRIOR APPLICATION NUMBER: US 60/261,766
| PRIOR APPLICATION NUMBER: US 60/261,766
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; ORGANISM: Homo sapiens
US-09-925-065A-611338
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                                                                                                                                                                                                                                                                          ; TYPE: DNA; Homo sapiens US-09-925-065A-611339
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SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 611339
LENGTH: 653
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SEQ ID NO 611338
LENGTH: 653
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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Local Similarity 38.5%;
nes 50; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 AUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCU 123
64 AUUGUUGGAAUCACCGUACCUAUUUAAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCU 123
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                                                                             ACAGCATGATGTTCCCATGGTAGTTAGAATTCTTACATGGTACAGGCTTCTAGGAGGCAC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCACTGTGT 168
                                                                                                                          ACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUGCU 63
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                                                                                                                                                                          Score 35.6; DB 4; Length 653; Pred. No. 0.43; Indels
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; ORGANISM: Homo sapiens
US-09-925-065A-151690
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US-09-925-065A-151690
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 219841, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151690
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                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.1.29
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum.
FILE REFERENCE: 108827.135
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
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APPLICATION NUMBER: US 60/167,363
                     APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 TACCAGTTAACAGAGAAGTGTTGGCACTAAAGTTACTACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AUCAAUAUCU 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 AGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACCU 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
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US-10-027-632-219841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 219841
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 219841
                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
-10-027-632-219841
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Best Local (
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TYPE: DNA
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Local Similarity 29.4%; Pred. No. 1.3;
hes 42; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-11-23
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APPLICATION NUMBER: US 60/167,363
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                                                                                                                                                                                UAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCC 101
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Pred. No. 1
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APPLICANT: Coonrod, Scott A
APPLICANT: Herr, John C
APPLICANT: Wright, Paul
TITLE OF INVENTION: Egg Specific Surface Proteins
FILE REFERENCE: 00498-07
CURRENT APPLICATION NUMBER: US/10/181,612
CURRENT APPLICATION NUMBER: US/00/181,612
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION WHERE: US/01/177,123
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 7
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US-10-181-612-3/c
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Publication No. US20030186369A1
                       NAME/KEY: misc feature
LOCATION: (2577)..(2577)
OTHER INFORMATION: "n" m
                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (2525)..(2525)
OTHER INFORMATION: "n" m
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LOCATION: (2481)..(2481)
OTHER INFORMATION: "n" meaning
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LOCATION: (2453)...(2453)
OTHER INFORMATION: "n" m
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LOCATION: (2382)...(2382)
OTHER INFORMATION: "n" meaning
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NAME/KEY: misc_feature
LOCATION: (2556)..(2556)
OTHER INFORMATION: "n" m
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NAME/KEY: misc feature
LOCATION: (2447)..(2447)
OTHER INFORMATION: "n" m
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LOCATION: (2340)..(2340)
OTHER INFORMATION: "n" meaning
NAME/KEY: misc_feature
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OTHER INFORMATION: "n" meaning
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OTHER INFORMATION: "n" meaning
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ORGANISM: Mus musculus
FEATURE:
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LOCATION: (2366)..(236
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RESULT 12
US-09-925-065A-91879
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; Publication No. US20050228172A9
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US-10-741-600-17662/c
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CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17662
LENGTH: 95832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17662, Application US/10741600 Publication No. US20050026169A1 GENERAL INFORMATION:
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Best Local (
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INPARCTION, METHODS OF DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: "n" meaning any nucleotide selected
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LOCATION: (2630)..(263
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OTHER INFORMATION: "n" m
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LOCATION: (2666)..(266
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                                                                                                                                                                                                      TTTAGTTTTGAATTTTCCTGTCAAAGCAGTTTAACTCATCAATATCATAATCTACCATCCA
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                                                                                                                                                              UAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGAAGAUUA 162
                                                                                                                                                                                                                                                                                                                       AACAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUGC 62
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                                                                                                                                                                                                                                                                                                                                                            16.8%; Score 32; DB 8; Length 95832;
29.4%; Pred. No. 56;
7ative 33; Mismatches 80; Indels
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
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PRIOR APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                 ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-925-065A-91879
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 91880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                   Matches
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 91880, Application US/09925065A Publication No. US20050228172A9
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CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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Local Similarity 44.4%;
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                                             16 UGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUU 69
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Pred. No. 13;
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Pred. No. 13;
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US-09-925-065A-91881 ; Sequence 91881, Application US/09925065A ; Publication No. US20050228172A9

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RESULT 15

US-09-938-842A-4112/c
; Sequence 4112, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
APPLICANT: Kreps, Joef
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Thu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4112
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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; NUMBER OF SEQ ID NOS: 957086
; SOGTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91881
LENGTH: 1626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-91881
                                                                                                                                                  Query Match
Best Local Similarity
Matches 37; Conserv
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
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157 AGAUUAGGUAGUCUCUAAACAGAA 180
                                                                                 97 GCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCUAGGAGAACUGUGCUAUGUUUAGA 156
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44.0%; Pred. No. 20;
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44.4%; Pred. No. 13;
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Search completed: December 22, 2005, 16:21:20 Job time : 444.264 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Maximum Match 100%
Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq3:*
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US-10-995-561-13273
US-11-117-187-201
US-11-117-187-201
US-10-750-185-60944
US-10-750-185-61-13263
US-10-995-561-13263
US-10-995-561-13277
US-10-995-561-13277
US-10-995-561-1227
US-10-750-185-42261
US-10-750-185-42261
US-10-750-185-48297
US-10-750-185-51618
US-10-750-185-51618
US-10-750-185-3761
US-10-750-185-3761
US-10-750-185-3761
US-10-750-185-3761
US-10-750-185-34698
US-10-750-185-44698
US-10-750-185-44698
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US-10-750-185-44698
US-10-750-185-44698
US-10-750-185-34698
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Sequence 13273, A
Sequence 201, App
Sequence 201, App
Sequence 45634, A
Sequence 45634, A
Sequence 13263, A
Sequence 13277, A
Sequence 40632, A
Sequence 40632, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 61632, A
Sequence 61632, A
Sequence 51618, A
Sequence 51618, A
Sequence 47497, Ap
Sequence 31807, A
Sequence 31807, A
Sequence 47483, A
Sequence 47483, A
Sequence 4753, A
Sequence 28553, A
Sequence 28553, A
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| RESULT 1 US-10-995-561-13273/c US-10-995-561-13273, Appli Publication No. US200 GENERAL INFORMATION: APPLICANT: CARGILL, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: CLOO CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE: NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ fo SEQ ID NO 13273 LENGTH: 95832 TYPE: DNA ORGANISM: Homo sapi | | 444 5443 | | 3210987 | 4 N O |
| JS-561-13273/c JCCe 13273, Application No. US2005027 AL INFORMATION: GANT: CARGILL, Mich GOF INVENTION: GENER GOF INVENTION: CAR S OF INVENTION: DET REFERENCE: CL001559 ENT APPLICATION NUMB SINT FILING DATE: 20 SIR OF SEQ ID NOS: 85 ARE: FastSEQ for Wi JNO 13273 JNO 13273 JNA HOMO Sapiens SILORA MISM: Homo Sapiens | | 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 999 |
| 1-13273/c 3273, Applic n No. US2005 FORMATION: IFORMATION: IFORMATION: IFORMATION: IFORMATION: IFORMATION: IFORMATION: INVENTION: IN | | 13.7 13.7 13.7 13.7 | 7888899 | | 14.1 14.1 14.1 |
| 0 H. ZH GX 50 | | 1696 2495 172649 190882 | 1434 387780 1494 1953 2240 40644 180654 | 600 695 1174 76589 317876 1082144 | 3572 86585 645179 |
| US/1099 94A1 94A1 POLYMC VASCULA TION AND 11-24 11-24 PMB Vers | | | | 7 | |
| ULT 1 10-995-561-13273/c equence 13273, Application US/10995561 ublication No. US20050272054A1 ENERAL INFORMATION: ENERAL INFORMATION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CL001559 CURRENT APPLICATION NUMBER: US/10/995,561 CURRENT FILING DATE: 2004-11-24 NUMBER OF SEQ ID NOS: 85702 SOFTWARE: FASESEQ for Windows Version 4.0 BO ID NO 13273 BO ID NO 13273 CORGALISM: Homo sapiens ORGALISM: Homo sapiens | ALIGNMENTS | US-10-750-185-54316 US-10-750-185-34514 US-11-121-086-36 US-11-121-086-69 | US-10-750-185-43316 US-10-995-561-13259 US-10-750-185-49364 US-10-750-185-37750 US-10-955-0548-69 US-10-995-561-13480 US-10-995-561-13480 US-10-995-561-13480 US-10-750-185-26208 | US-10-750-185-4062 US-10-623-155-39 US-10-750-185-45653 US-10-995-561-13322 US-10-995-561-13227 US-10-975-187-21 US-10-750-185-28788 | US-10-793-626-3988 US-11-117-187-198 US-10-995-561-13293 |
| RESPONSE, METHODS | | Sequence 54316, Sequence 34514, Sequence 36, Ap Sequence 69, Ap | 1329 1329 493 69, 1348 58, | 4062 39, 4565 1332 1322 e 211 | Sequence 3988, A Sequence 198, Ap Sequence 13293, |
| of Sc | | le, A le, A Appl Appl | | עכנד ע | App App 3, A |

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US-10-750-185-21629; Sequence 21629; Application US/10750185; Publication No. US20050260603A1
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-201
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US-11-117-187-201/c
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
       APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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SEQ ID NO 13305
LENGTH: 50353
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TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REPERENCE: ARCD: 309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
                                                                                APPLICANT:
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PREUSS, DAPHNE APPLICANT: COPENHAVER, GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001559
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 80450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56544 GAAGAAGAAATATTCAATATATTCTTCGAGTATCTATGTTATAGAAGTCAATGTTAC 56485
                                                                                                                                                                                                                                                                                                                                                                        56484 TACTTTTGGTTCTACTCCTTGGGTATTGGATACCA 56450
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                                                                                                                                                                                                                                                                                                                                                                                                                     84 UAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCA 118
T: ROSENFELD, David
T: HOLM, Tom
T: BATES, Stephen
T: FANTIN, Dennis
T: FANTIN, COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 GAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCACCGUACC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 AGUGCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGCTATGATTATATCATACCGGGTTACAATGTGGAGCAAATTAGGTAAT 37597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGATCTTGGATTÁATTÁCTAAÁCCTTTCTGAGCCTTGGTTTCCÁCÁTCTGGAAAAAGC 37648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.5%; Score 29.4; DB 7; 35.8%; Pred. No. 9.7; tive 20; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 80450;
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RESULT 6
US-10-750-185-45634
) Sequence 45634, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: BOVING MMBT03382
US-10-750-185-21629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 60944
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                  APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: MMI1100-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                        430 TITTTCTGTCCAGATTACCTGTCTATGGTTCCATTC 465
                                                                                                                                                                                                                                                                                                  370 CAACATTAACTTGTTTGATTACTAAGAAGTTTTAAATATTAAAAACTGTTAAAAGTGCAT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 TTTTTCTGTCCAGATTACCTGTCTATGGTTCCATTC 183
                                                                                                                                                                                                                                                       65 UUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUC 100
                                                                                                                                                                                                                                                                                                                                                                                        33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 UUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUC 100
                                                                                                                                                                                                                                                                                                                                           5 CAAUGUGAUCUUGCUUGCGGAGGCAAAAUUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUA 64
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                                                                                                                                                                                                                                                                                                                                                                                   h 15.2%; Score 28.8; DI Similarity 34.4%; Pred. No. 2.8; Similarity 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1209;
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Sequence 13263, Application US/10995561

| Publication No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| FILE REFERENCE: CL001559
| CURRENT APPLICATION NUMBER: US/10/995,561
| CURRENT APPLICATION NUMBER: US/10/995,561
| CURRENT FILING DATE: 2004-11-24
| NUMBER OF SEQ ID NOS: 85702
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 13263
| LENGTH: 57198
US-10-995-561-13277/c
Sequence 13277, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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; ORGANISM: Bovine 19866881349204
US-10-750-185-45634
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; ORGANISM: Homo Bapiens
US-10-995-561-13263
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                                                                                           RESULT 8
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SEQ ID NO 45634
LENGTH: 2874
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIO0-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1797 CAPATGATCTCAGCTCAGATATGCATAAAGAGTTTCCCAAGTACACCAGCAAGAATA 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1857 GCCATTTAAAGGTCTAAGAATTGTGTTAAACCTTAAAACACCAAAATCAATAGACAGCAGC 1916
                                                                                                                                                                                                            134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                     74 UCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCU 133
                                                                                                                                                                                                                                                                                                                                                                                            14 CUUGCUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUGGAA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                          GTACTGTACATAGTTAATTATTTCATCTAAGTTGTGTGAGCCAAACCTGTGAATTACT 28714
                                                                                                                                                                                                                                                                                                                                              GCUAUUGUUGGAAUCACCGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGC 120
                                                                                                                                                                 ATTCATGCAGGGCAATGATGATAA 28690
                                                                                                                                                                                                          AGGAGAACUGUGCUAUGUUUAGAA 157
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BATES, Stephen
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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38.3%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.2%; Score 28.8; 34.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 57198;
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; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METI
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT FILING DATE: 2004-11-24
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FAStSEQ for Windows Version 4.0
; SEQ ID NO 13277
; LENGTH: 173995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13277
                                                                                                                                                                                                                                                                                      APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
VMMBER OF SEQ ID NOS: 64922
SOPTWARE: Patentin version 3.1
SEQ ID NO 40632
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                                                                                                                                                                                                                                         ; LENGTH: 952
TYPE: DNA
; ORGANISM: Bovine 19866880791528
US-10-750-185-40632
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US-10-750-185-40632
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                                                                                                                                                           Query Match
Best Local S
Matches 42
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APPLICANT:
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                                                                                                                  35 UGCĄCĄGUĄUĄĄĄĄUCUGCĄĄGUĄGUGCUAUUGUUGGĄAUCĄCCGUĄCCUĄUUUAGGUUU 94
                                                                                                                                                               42;
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KERR, Richard
ROSENFELD, David
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                                                                             TCCACGGTAAAGAATCTGCCTGCAGTGCAGGAGATCCAGGTTCGGTTCCTAGGTTGGGAA 827
                                    ACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLM, Tom
                                                                                                                                                               Conservative
                                                                                                                                                           14.9%; Score 28.4; DB 6;
44.7%; Pred. No. 3.4;
tive 11; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Indels
                                                                                                                                                               41;
                                                                                                                                                                                                    Length 952;
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RESULT 10 US-10-750-185-42261

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FILE REFERENCE: 64991
CURRENT APPLICATION NUMBER: US/10/860,501
CURRENT FILING DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 12
SOPTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 1891
TYPE: DNA
ORGANISM: NUS musculus
US-10-860-501-2
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 42261
SEG ID NO 42261
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TYPE: DNA
; ORGANISM: Bovine 19866881270808
US-10-750-185-42261
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Publication No. US20050271638A1
GENERAL INFORMATION:
APPLICANT: L1, Linheng
APPLICANT: He, Xi
TITLE OF INVENTION: BMP PATHWAY METHODS AND COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Publication No. US20050260603A1
GENERAL INFORMATION:
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, FARAN' KER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 14.8%; Score 28.2; DB 6;
Local Similarity 36.4%; Pred. No. 5.3;
nes 44; Conservative 19; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 14.9%; Score 28.4; D)
Local Similarity 35.9%; Pred. No. 4.3;
1es 51; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                            1211 CCTGAAGAGCAAAAACATCCTTATTAAGAAAAATGGAAGTTGCTGTATTGCTGACCTGGG 1270
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                                                                                                                                                                                                                                                                                                                                             18 CUUGCGGAGGCAAAAUUUGCACAGUAUAAAAUCUGCAAGUAGUGCUAUUGUUGGAAUCAC 77
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                                                                                                                                                                           CGUACCUAUUUAGGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCUAGGA 137
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                                                                                                 CCTAGCTGTTAAATTCAACAGTGATACAAATGAAGTTGACATACCCTTGAATACCAGGGT 1330
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; TYPE: DNA
; ORGANISM: Bovine 19866880368423
US-10-750-185-48297
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US-10-750-185-48297
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Publication No. US20050271638A1
GENERAL INFORMATION:
APPLICANT: Li, Linheng
APPLICANT: He, Xi
TITLE OF INVENTION: BMP PATHWAY METHODS AND COMPOSITIONS
FILE REFERENCE: 64991
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 48297
LENGTH: 1946
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Publication No. US20050260603A1
GENERAL INFORMATION:
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LENGTH: 2056
                                                                             Matches
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CURRENT FILING DATE: 2004-06-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mus musculus
                                                                   y Match 14.6%; Score 27.8; D)
Local Similarity 34.5%; Pred. No. 7.4;
hes 41; Conservative 21; Mismatches
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144 TGGTAGTAGAAAACTGGCTAATTATGTTATTCCTTCAAACCCTGTAGAAAACAGCCCCTC 203
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KERR, Richard
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: RESR, Sichard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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US-10-750-185-61632/c
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SEQ ID NO 61632

LENGTH: 1223

TYPE: DIA

ORGANISM: Bovine 19866881420:

US-10-750-185-61632
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US-11-092-140-101
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Publication No. US20050262590A1

GENERAL INFORMATION:
APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.
TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthes
FILE REFERENCE: 16515.054
CURRENT APPLICATION NUMBER: US/11/092,140
CURRENT TELLING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US/09/688,069
PRIOR FILING DATE: 2005-01-14

NUMBER OF SEQ ID NOS: 114

SEQ ID NO 101
LENGTH: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 61632, Application US/10750185 Publication No. US20050260603A1
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                                                                                                                                             Query Match 14.5%; Score 27.6; DB 6; Length 1223; Best Local Similarity 33.6%; Pred. No. 7.1; Matches 49; Conservative 23; Mismatches 74; Indels 0
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                                                705 AAATTGGAAGATTCTAAAACCTTGCTTGAGTGCTCTACTGTTGATTTCTCCCGAGGAGTAA 646
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                                                                                                 30 АААИИИGCACAGUAUAAAAUCUGCAAGUAGUCCUAUUGUUGGAAUCACCGUACCUAUUUA 89
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  90 GGUUUACGCUCCAAGAUCGGUGGAUAGCAGCCCUAUCAAUAUCUAGGAGAACUGUGCUAU 149
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Search completed: December 22, 2005, 16:41:12 Job time : 176.374 secs

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Maximum DB seg length: 200000000
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Match
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BD173517 Novel ter BD177021 Novel tra AF022937 Rhopalosi AC108007 Homo sapi AC050860 Homo sapi AF535531 Aphid let AX763949 Sequence AC110859 Rattus no AC118859 Rattus no AC118859 Rattus no Continuation (159 AC079853 Oryza satt CR383679 Danio rer CR388405 Zebrafish Continuation (5 of CR847526 Danio rer GR45920 Danio rer GR45920 Danio rer GR4518 Z6563_1 Zeb
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| 1 | 31JAN-2001 WO 2001JP000641 25JAN-2001 JP 01F 016746 NOBUHIKO NAKASHIMA, YASUSHI KAN CLI2N15/11, C12N15/86, C12P21/02 NOVEL tertiary structure havir translation activity Key Location/Quali source /organism='Rho Location/Qualifiers 1. 175 1. 175 /organism="Rhopalosiphum F /mol_type="genomic RNA" /db_xref="taxon:66834" | PATENT: WO 02061080-A 7 08-AUG-2002; JAPAN AS REPRESENTED BY DIRECTOR GENERAL OI SERICULTURAL AND ENTOMOLOGICAL SCIENCE MIN: FORESTRY AND FISHERIES, NOBUHIKO NAKASHIMA OS Rhopalosiphum padi virus PN WO 02061080-A/7 PD 08-AUG-2002 | licistroviridae; (bases 1 to 1; Nakashima,N. and Novel tertiary st | 7377CH | સ | | 56796 189 189 4158 9264 | 01500 63093 01429 | 268294 5853 161393 | 1140 02971 09742 | 39986 60006 12430 | 77531 | 25911 79428 | 94001 | 10000 | 3 |
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| , | 2001P000 01P 016 5/86,C12P structure trivity Location 1. 1.7 /organis alifiers Rhopalosi Rhopalosi Raxon:6683 | AT DE OFFICE A PROPERTY A PROPERT | ori, | - 15 E | | ΑI | C09 1173 1177 1177 1002 | 645 | 645 | 7281 7875 | X C C C | X92 | 7892 7892 | 115 | P00 | į |
| | 2001JP000641 01P 016746 1IMA, YASUSHI KAN 5/86, C12P21/02 structure havin tivity 1175 1175 /organism='Rho alifiers Rhopalosiphum p genomic RNA" axon:66834" | -AUC RECT ICA BUH: TUS | vs. ,Y. having | strand | 175 bp having | ALIGNMENTS | AC099183 BD173513 BD177017 AB002529 AF014388 | 807 544 937 | AC155761 AX283321 AL645966 | 055 994 | 715(895) | BX005396 BX927305 BY890568 | 588 | 125 | 485 821 | ; |
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OS Rhopalosiphum padi vi...
PI SHERIES
OS Rhopalosiphum padi vi...
PN JP 2002306168-A/7
PN JP 2002306168-A/7
PD 22-CCT-2002
PP 25-JAN-2001 JP 2001016746
PI NOBUHIKO NAKASHIMA, YASUSHI KANAMORI
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02// PC
(C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC
(C12N15/09,C12R1:92),C12N15/00,C12N15/00,C12R1:92) CC
Novel translational activity-promoting higher-order structure FH
Location/Qualifiers
1. .175
1-m-'Rhopalosiphum padi virus'.
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AF022937
Rhopalosiphum
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1 (bases 1 to 175)
Nakashima,N. and Kanamori,Y.
Novel translational activity-promoting higher-order structure Patent: JP 2002306168-A 7 22-0CT-2002; DIRECTOR GENERAL OF NATIONAL INSTITUTE OF SERICULTURAL AND ENTOMOLOGICAL HIROSHIMA PREFECTUAL INDUSTRIAL TECHNOLOGY PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION, SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE MINISTRY OF AGRICULTURE FORESTRY AND CREATURE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE TO THE PROMORGANIZATION SCIENCE T
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175 bp RNA linear
Novel translational activity-promoting higher-order
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                                                                                                                                                                                                                                                                                                                                                                                              CTTGGTTAGCTATTTAGCTTATCAATCAAGACGCCGTCGTGCAGCCCACAAAAGTCTAG
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/mol_type="genomic RNA"
/db_xref="taxon:66834"
10011
padi virus comp
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                                         VRL 16-DEC-1998
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USDA-ARS-MWA-CPRU, 1102 S. Go
Location/Qualifiers
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Direct Submission
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NMRLRKILPRVKYQYTEPSUDVISSVSPTKSGISIDKIILDNVNLEEQRAWPEMDKSVET
I VNHVYYPNTVYMTANKNDGTETNIGHIIFIGOGVALMPYHYKIAIEERQYQSVULYS
I VNHVYYPNTVYMTANKNDGTETNIGHIIFIGOGVALMPYHYKIAIEERQYQSVULYS
RKLIGAKIPSSVEDTFVRLQGKDAMIWAFPVTVNSFKNIVSHFVDIGSYPLVPSCPGI
LAKYYFANAETEKSRVCISAIGVSERDEVDVMSVPGCMEIVRNRDFYTYTAPTRAGDC
GAALCVANTCIQGKIVGIHVSGVEGLCKGNSSAITKQMIEESLKKMPSIAQYAYPSSA
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QEYTAPLDLTVILDSTNWYKIGKCSAVIVARDTLKACLRELALHPEHIDSQYRSIITE
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MADWYDLNWDYVEAHKRNVVGGQVLLKDEYLDYLRRLYYECVHHLHIMNFKQGSLMYY
VRNGIPSGCPVTAPLNSIVNQMALVYCWYHIIDDPLKRNVKEFPEHTSSVFYGDDFVM
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GEIIDERILGRKKYGKERPVLDQNIVNDIRDGLKSVYKQSHEXEBEYYKKPITFOQAI
LGINGDPFIKSLDRNTARGFPYSTMEKGTKGKTKTLWFGNGMDVDLTGPYAAJARADVS
LETDILNGTRPEIVMTDTLKDQKIAIAKANAGKTRLFSAAPMHYAIALRKVCAPFVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESLINCIPEĂVURR I IPBĄPINURĮ I VPBYQMEYMSANGDKI, YRLDAKKARQDEGDULCIPEVY REDLEDASSRRNI I IPDĄTYTEVYKLCODMYNIADYANIDYANILEX YRKKOVĄCYEK KETDDS YNGASTLVETSTĄCYHLDDVTINLU ILOPS YMKRLYMNI CKRYYSTRLMISKT DMSAPEMLLRGDROGAYDKCI, SI URBTRCELINSMI INRETEVI KUVEGNYWPLFKACAG DASA FEMLLRGDROGAYDKCI, SI URBTRCELINSMI INRETEVI KUVEGNYWPLFKACAG DASA FEMLLRGDROGAYDKCI, SI URBTRCELLITIM KANBECIDERNICKKCHKAVDLC VKWYTKCHCYALHMEKAÇVNILKY YTAAAMY OBE PMIKBERECVELLTI II DOLCSCOLO VKWYTKCHCYALHMEKAÇVNILKY YTAAAMY OBE PMIKBERECVELLTI II DOLCSCOLO VKWYTKCHCYALHMEKAÇVNILKY YTAAAMY OB PMIKBERECVELLTI II DOLCSCOLO VKWYTKCHCYALHMEKAÇVNILKY YTAAAMY OB PMIKBERECVELTI II DOLCSCOLO VKWYTKCHCYALHMEKAÇVILKY YTAAAMY OB PMIKBERECVELTI II DOLCSCOLO VKWYTKCHCYOLONIK YTAAAMY OB PMIKBERECVELTI II DOLCSCOLO VKWYTKCHCYOLONIK YTAAAMY OB PMIKBERECVELTI II OLCSCOLO VKWYTKCHCYOLONIK YTAAAMY OB PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLCSCOLONIK YTAAAMY OR PMIKBERECVELTI II OLGSCOLONIK YTAAAMY O
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                                                                                                                                                                                                                      join(7103. .7105,7107. .9560)
/note="the site of translation initiation could not be determined from the nucleotide sequence, but may invol-
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ILMFCINIERVPLRCYKFSANVNMKVALSQLFVLMAALVNKERLSDQYDFLFVLQNFL
HFFFRNLSYTNPIDLIEHSFIHELGLYCAKLVMIRPISTTEYVLGGDWDFDKFVLASK
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/protein_id="AAC95509.1"
/db_xref="GI:2911299"
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/mol_type="genomic RNA"
/db_xref="taxon:66834"
    translation="MPANINENTTTKIQQQILSFSSEGESPSSSTVLAPLKLQDPILD"
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., God, S., Goyette, M., Graham, L., Grand-Pierre, N., Galago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., MeEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McEwan, C., McCarnan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogevtti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Storavers, M., Travis, N., Trejillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zannoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone CTD-3038L12
Unpublished
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AC108007
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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HLOSLERTDSDEMSIDYVARTYNYVSRFMI KONGPOTIVLYSHYVSFTSWFIEVGITG
LSIPHLYFAASNPVLMRGGMI KLKFVKTKFHSGRVRI LYVPGFFGGTIPINFETDAN
YSTVVDLRSDTDVEFNVPYVATIVFMLHVNSTPMYTAFSQIHACRSI VVEVLNELUNTS
TVSDTIEVLVEVCAAEDI EFAI PI VPSLTPRAAPQGSRRTAYDLITSI AQVGTDTGD
TPLEVSREEPTTENDVPLQPTTTTPNASNLMMGEKVTSFRQLIKAFSAI TPPTQNRY
EFTQFFMINTNRLEGVTQEGSSDIDGISWFASLYAFYSGRMXKIAFLSANASPLVVAL
KRNSLYSGVRVLDTNGTWTYPDYKGAEVFMTPNBGIHELSI PYYSSYPVTLTTYNSTD
SDVLDARNGFNRVI ARPHSDTSAYVYRAAGDDFSFGFLLGAPIVI IGLSSVRLICVKY
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IDLSTTTEATMTIPFVSPFLYYNLVTGSGDIGTFQLIVYSPLVDLVSGGNIDYTIWVN
MTNVRTEFFTGMPTSIAQVGEEGSTQQKQGFVTRQSEAYSTIMEPLTKIPGVGQLIGY
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Barran,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,J.
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge
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Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Only the first 91.9 kb of this clone are being submitted.
The remainder overlaps accession number AC055860 [WICGR project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
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/rpt_family="L2"
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complement (29002. .29304)
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                                       Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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Research, 320 Charles Street, Cambridge, MA 02141, USA
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Homo sapiens chromosome 11, clone RP11-195023, complete sequence.
AC055860
AC055860.13 GI:17985932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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1 (bases 1 to 160494)
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                     (bases 1 to 160494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 160494)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(TG)n"
complement(31075...31197)
/rpt_family="MIR"
31198...31246
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32030. .32230
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/rpt family="MSTA"
30412 .30452
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31822
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  Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="(CA)n"
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| repeat_region 48914919 | | /rpt_family="MIR" | repeat region complement(43164410) | repeat_region 42674315 | repeat_region complement(41444266) /rpt family="MIR" | /rpt_family="(TG) | | repeat_region complement (24102828) | repeat_region complement(20752377) /rpt family="AluJo" | /rpt_family="MIR" | comp. | repeat_region complement (8701103) | repeat_region complement(569869) | repeat_region complement(524568) /rpt_family="MER41C" | | region | | /clone="RP11-195023" /clone="RP11-195023" | /map="11" - 1-1 /map="11" - 1- | /db xrefe"taxon:9606" | /organism="Homo sapiens" /mol type="genomic DNA" | rce 1160494 | FEATURES Location/Qualifiers | | Project Information Center project name: L9785 | Reb Bite: http://www-Beg.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu | | Center: Whitehead Institute/ MIT Center for Genome Research | http://ftp.genome.washington.edu/RM/RepeatMasker.html | All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) | COMMENT On Dec 28, 2001 this sequence version replaced gi:17223377. | | TITLE Direct Submission | Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., | Tophan, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., | Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straugg, N., Subramanian, A., Talamag, J., Tegfave, S., Theodore, J., | Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., | Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond.C. Retta R. Rieback M. Rilev.R. Rise.C. Rogov.P. | Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., | <pre>McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus.L., Mihova.T., Mlenga.V., Murphy,T., Naylor,J., Nguyen,C.,</pre> | MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., | Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Liu, G., | Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., | Perreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., | Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., | Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., |
|------------------------|---------------|-------------------------|------------------------------------|------------------------|--|-------------------------|---|-------------------------------------|--|-------------------|------------------------------|------------------------------------|--|---|---------------|---|---|--|--|---------------------------------|---|-------------------------|------------------------------------|---------------|--|--|----------------------|---|---|---|---|-------------------------------------|-------------------------|--|---|--|--|---|---|--|---|---|--|---|---|--|
| | repeat_region | repeat_region | repeat_region | | repeat_region | repeat_region | repeat_region | | unsure | unsure | unsure | | - | repeat_region | repeat_region | repeat_region | | | repeat_region | repeat_region | repeat_region | | repeat region | repeat_region | repeat_region | | 1000001 | repeat_region | repeat_region | repeat_region | | repeat region | repeat_region | repeat_region | 1 | repeat region | repeat_region | repeat_region | | repeat region | repeat_region | repeat_region | Tobear_regroup | | ר דבססססד דבססססד | repeat_region |
| /rpt_tamily="L2" | 1987220070 | complement (1930919563) | <pre>/rpt_family="AluJb"</pre> | - | /rpc_ramity="insic" complement(1843018991) | complement (1805518429) | <pre>complement(1758818054) /rpt_family="L1ME1"</pre> | /note="<30 qual SNGL region" | /note="<30 qual SNGL region" 1741217416 | 1737817382 | /note="<30 qual SNGL region" | /rpt_family="AluSx" | <pre>/rpt family="L1ME1" complement(17294 17587)</pre> | /rpc_ramily="L2" complement(1723217293) | 1704717207 | <pre>complement(1692017030) /rpt family="MIR"</pre> | = | /rpt_family="L2" complement(1546116275) | 1474415124 | 1455714722 /rnt family="MTR" | 1423514533 /rpt family="AluJo" | /rpt_family="AluJ/FLAM" | /rpc_ramity="MBR208" 1321913317 | 11946 12060 | 1163011945 /rpt family="AluY" | /rpt_family="MER20B" | /rpt_family="MER65C" | / 10 | 1103611159 | /rpt family="AT rich" | /rpt_family="AluY" | /rpt_tamily="AT_rich" 1074010997 | 1057610610 | complement (1026610552) | /rpt_family="AluJb" | <pre>/rpt_tamily="MIR" complement(9605, .9915)</pre> | | 78428083 /rpt family="AluJo" | т. | /rpt_family="AluJo" 78117841 | 7691. 7810 | 74597653 /rot family="L1M4" | /rpt_family="L2" | /rpt_family="MIR" | /rpt_family="MERSA" | 50995299 |

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RS. Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barran, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Choepel, Y., Colangelo, M., Collins, S., Collins, Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collins, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Bardord, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McPhy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Fieback, M., Santos, R., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Suravers, M., Travis, N., Trigilio, J., Vessiliev, H., Viel, R., Vo, A., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Strauss, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vsasiliev, H., Viel, R., Vo, A., Wilson, B., Wilson, B., Straus, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
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Birren,B., Nusbaum,C. and Lander,E.
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Homo sapiens chromosome 11, clone RP11-113D6, complete sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/rpt_family="Allub"
complement (21855...22148)
/rpt_family="Allub"
complement (224444...22752)
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complement(21547. .21
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20601. .20834
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20445. .20599
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CE 4 (bases 1 to 172939)

RS Birren, B., Musbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Choepel, Y., Collymore, A., Comarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Lilu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, T., Naylor, J., Neneus, L., Mihova, T., Mlenga, V., McConnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Scange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Stombek, L., Zimmer, A. and Zody, M.
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Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zember, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zodva M. Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L., Zembek, L., Zimmer, A. and Zembek, L., Zimmer, A. and Zembek, L.,
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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------ Project Information
Center project name: L12764
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                                                                                                                                                                complement (678. .810)
/rpt family="Charliel"
complement (879. .1057)
/rpt family="LIM4"
complement (1395. .1513)
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/mol_type="genomic DNA"
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/db_xref="taxon:9606"
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'note="<30 qual SNGL region"
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complement(17827. .17929)
/rpt family="MIR"
18993. . 1992
/note="<30 qual SNGL region"
complement(21118. .21398)
/rpt family="AluSx"
21147. .21147
                                                                                                                                                                                                                                                                                                  complement (16607. .16612)
/note="<30 qual SNGL region"
complement (16746. .17360)
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11839. 12000
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'note="<30 qual SNGL region"
2672. 2788
2672. 2788
/rpt_family="5S"
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complement(16587. .16598)
/note="<30 qual SNGL region"
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complement(11344. .11683)
                                                note="<30 qual SNGL region"
0879. .20883
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t family="1"
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.17664
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Tement(9265. .10
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family="LTR41"
lement (8308. .8611)
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_family="LTR41"
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Van Munster,M., Dullemans,A.M., Verbeek,M., Van Den Heuvel,J.F., Clerivet,A. and Van Der Wilk,F.
Sequence analysis and genomic organization of Aphid lethal paralysis virus: a new member of the family Dicistroviridae J. Gen. Virol. 83 (pt 12), 3131-3138 (2002)
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Aphid lethal paralysis virus,
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Aphid lethal paralysis virus
Viruses; seRNA possitive-strand viruses, no DNA stage;
Dicistroviridae; Cripavirus.
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van Munster, M., van
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Research International, P.O Box 16, Wageningen 6700 AA, The
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                                                                 LNAEFRTY I QLI KQMTNNPNI RNAFI DMI FAPYVTAFNFTTDADI TESGSSETLQYLN
TLYINKLSALAQVGLNPNHAI TVDINILELA INKSLIWFADLIVALI SDKLQETVADYQR
TLYINKLSALAQVGSTRKMDLQDL VVNVFGALGSAGI ASSLVAQLVTSLRAYFVAPI
KI VALI TTI YNLYRFSTRKMDLQDL VVNVFGALGSAGI ASSLVAQLVTSLRAYFVAPI
AQI OTGSHLLI LKALSI TMFCLFI KQLFGKNTI DEFVTRLDR FFKAI SCLESMMSKLD
VVVKQI YTFMEEI LKKHNRFNNTDMLQDVLDWASEVEKYLELANRNEI KRDPATVLAA
                                                                                                                                                                                                                             /product="nonstructural polyprotein"
/protein id="AAN61470.1"
/protein id="AAN61470.1"
/db_xref="GI:24431319"
/translation="MSGTFSTTLPQLKLQLSIPELTQLKIRDAQAHEKPRIVAQLTRS
/translation="MSGTFSTTLFQLKLQLSIPELTGLKIRDAQAHEKPRIVAQLTRS
SKLYPRGVRLIKECTQLKLSPANLNLIRSLLPATKQLADEAIKSGALKQALRPEPLIV
WFCGKSGMGKTGMSYPFMMDMMRVFGDIPTDFQKNIYGRVPETEYWDGYTDQEYIIYD
DAFQIKDNVLKPNPELFEIIRLGNAFPVMLHMASVEEKNNTFANPKCVLLTSNLDRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="probably A; possibly G"
21153. .21158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="<30 qual SNGL region"
21144
                                                                                                                                                                                  LYLDYLMQHTKTHAQTKDCFFLMLKAIAMAKEHIFIEDGSFYSIAIALRLINASLATI
LNKPDMLKFTNLFRYCRLIRNFLKNRIISNSVTLTGLLLPRKYTIDCFKQSAVANNII
                                                                                                                                                                                                                                                                                                                                                                    RNA-dependent RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Aphid lethal paralysis virus"
/mol_type="genomic RNA"
/db_xref="taxon:209529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="probably T; possibly C"
21160. .21167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="probably A; possibly G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                            note="encodes putative helicase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.0%; Score 36.8; DB 8; 46.9%; Pred. No. 0.22; tive 17; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                       .6647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van den Heuvel, J.F.J.M. and van der Wilk, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9812 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         op RNA lin complete genome.
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VERSION
KEYWORDS
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DEFINITION
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   AUTHORS
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Best Local
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                                                                                                                                    ORGANISM
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                                                                                                                                Aphid lethal paralysis virus Aphid lethal paralysis virus
                                                                                                                                                                                                                                                              AX763949 9829 bp
Sequence 1 from Patent WO03040177.
AX763949
van der Wilk, F. and van Munster, M.
                                                                                                                                                                                                                               AX763949.1
                                                                   Dicistroviridae;
                                                                                           Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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PIDĀQRSIPĒQDKGSIVIĀRDVYRNLFRFTVVLNENGTĒKRĒGQIEMI
KHFLYWEHFVETFGSECKIPVLENGSNĀISBLIPGSVILĀGENHVKDPĀRBIĀ IVO
LPTNIGGFĀQĀYKHIIDĒQDLĀRVSDSPĀILĀRVQNĀSĒRDRRĢGTNYVREIFWLSTĀ
TPĒDĒHLVESTVĒĒANVVVQNRGSYTYHĀVTFFGDGSILIĀSNĀĀTTQKIMGMIĀGI
THMNKGISVALTRQIIDĒLMKHPQPISQYGHEIVPLDUHVENGTFLIYGTĒLGR
RIMGSVKTĀLĒKSPĀYGKLIESPNKFGYLRPFTDENGTTIDĀWTLQRNKYGVRĀPYPS
QQRUDĀVYĒĀMSVFYQREYINSPĀHYKLPLTRĒĒTIVGINGDPFINĀINRQTĀPGYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNYARPALWISNTIRDVAKHFOWSKPTTAEAHHLNKLTGSRFMANADGVDMSHSLGIS
AINELEVNPALTRTDIDEMTVAHIARTPOFIKKROWTSNGKAGDVLYATPITPSFFSI
AVDSTRVABSHLAYISSPETMWRGGINFHFKFVWTKEHSGRVEILFVPGDYSNDDKLP
DNADPNASYSSVVDLRSDTDVTFNVPFVSVQFWKLSSADVTSPLKDYQHSVGRLYVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDDGRNHSIIDFLQRFINIQNIEWSTNDNAGKTLMAVDLPLDFIINNSMYKAKCERFY
GFRADVELKLQVNAQPFQAGRLLLVYIIGOYKYIGEDGKYYDGBRINVDDASLVFLTGS
PRVDLDLSTCTPATMCVPYYSBYLFSDLTMGVHIIGRFKVVVYSDLVDGASSGIVDT
LMINFKNIKIKYPTAMPIAATAQVGTEAIQDSAGAGVISSAAASVSSVLSPLQDVPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYEKEGKSGKTKWFGDGMDYDLINDACKQLMADVDELAQCMLDNVRPRIIWIDTLKDA
KIPIAKANVGKTRIFTACCHIVIILEGA
LLAKRUCKKRIGHTACCHIVIILEGA
LLAKRLKRUGKRIVAGDYSUNPOCTLPVQYVEVAVKINVDWFMENWDQIVAADRHVING
RELDYDEFEQFLMKIGVECINHLHIANHSDLTGAALIYVRNGIPSGCPATAILNSIV
MHCCLADSWLDIMDGTPYATWASFFEHTSSIFYGDDFINNIREBVIDVNQETLTPVL
KKNLEMTMTDBAKTGEKVKARTLESUSFLKKKERFESFVGLWVAPIDIDVNQETLTPVL
KKNLEMTMTDBAKTGEKVKARTLESUSFLKKKERFESFVGLWVAPIDIDVNQETLTPVL
KKNLEMTMTDBAKTGEKVKARTLESUSFLKKKERFESFVGLWVAPIDIDVNQETLTPVL
KKNLEMTMTDBAKTGEKVKARTLESUSFLKKKERFESFVGLWVAPIDIDVNQETLTPVDSRS
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QFVKQAVLVGVSVFSTYMCVKVSFALGDYVKGKIVFKYISDNDQVAQLVSEANACFDK
GCNNCKLCKNAAMNQLNVKWNSSCLCYVKRMEKGKDMINKYAISLYGDQRVSNNHELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVYAARIRLIPENGATEANAGPVQEDNTVIDETRTAADVYMPRNLEGTFEFQVPHYSR
YPLLPNTAGSIPVIGVQDLIQRNLVSVNILTEAETTKALFYRAVGDDFSFCGLLGPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNELRATSTVSDTISCLVEVSGASDFELSMPRQPKIYPTLRAAKSTTLNRVIRGIAQV
NVAESTPVSPEIIQKTGEVGESSMRQPQGTSFTSSALTVGEKVTSLRQILKRFHLIYS
NLTTSTKNNNLYRINSFKTPKPIAAQATMVNIDLYSYYSYIFAYYRGSFRFKIAPFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      determined"
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YDMTKQISNTLPSIIKNPELKRLIDSHARVYDNAVSRRANSTRIVGHGATYDARPRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNNLDVYRFTKFSAFDGRTIETDMTYAQVTEECSMKMASRFNQHMDFTNYLDAYRNPT
YEPEDIVEHPIDAEAQIGNAARVAAGNVAGFLVTNHCLRKYVHGDDDTILMALLRKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="capsid protein precursor"
/protein_id="AAN61471.1"
/db_xref="GI:24431320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTLLKLRNEELGGDFEINY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="PANFQETQMTHEQQQILTFSSEGMTPSTSIYTDPLDLDMSYLTS
                                                                                                                                                                                                                               GI:32258304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%;
                                                             Cripavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB Pred. No. 0.71; S; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                              RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9812;
                                                                                                  DNA stage;
                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                              PAT 25-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
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CDS

RESULT 8

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SOURCE
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AC107353
LOCUS
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KEYWORDS
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RS Allen, C., Allen, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, Metzker, M.Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Bazber, M., Barnstead, M., Benahmed, F., Blaiwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Belawalo, K., Blair, J., Blarkenburg, K., Blyth, P., Brown, M., Belawalo, K., Blair, J., Blarkenburg, K., Blyth, P., Brown, M., Chen, X., Chen
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Patent: WO 0304017-A 1 15-MAY-2003;
Plant Research International B.V. (NL)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RATTUS norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC107353.4 GI:23101281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-47B12, ****, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 240387)
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/mol_type="unassigned RNA"
/db_xref="taxon:209529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240387
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2, *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 08-OCT-2002
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On Sep 18, 2002 this sequence version replaced gi:21737464.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walse, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, G., Wallson, R., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Zhou, X., Zhang, J., Zhou, J., Zhou, X., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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Direct Submission
Submitted (19-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 240387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doce/Genbank_draft_data./NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                 be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990329
Consensus quality: 209782 bases at least Q40
Consensus quality: 213003 bases at least Q30
Consensus quality: 213005 bases at least Q20
Estimated insert size: 232384; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH230-47B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor Co
Center code: BCM
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/organism="Rattus norvegicus'
                                                                       Location/Qualifiers
                                                                                                            171950: contig of 171950 bp in length 172050: gap of unknown length 240387: contig of 68337 bp in length.
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KEYWORDS
SOURCE
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RRS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Banbarianaike, D., Barber, M., Bacas, E., Baden, H., Bendaranaike, D., Barber, M., Barnstead, M., Bendahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Belaikenburg, K., Blyth, P., Brown, M., Bendahmed, F., Barder, M., L., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Cardens, V., Carder, R., Carderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., DrSouza, L., Cackroll, M., L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davis, G., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davis, G., Dava, A., Durbin, K., Duval, B., Eaves, K., Durah, A., Durbin, K., Duval, B., Eaves, K., Durah, A., Durbin, K., Duval, B., Eaves, K., Degan, A., Bacctto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fransder, S., Garcia, A., Garner, T., Garza, M., Gebregocrgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Guevrar, W., Guwarat, W., Gharrath, F., Hangland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Johnson, R., Jolivet, A., Kapathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Lu, X., M., J., Loudon, P., Longacre, S., Lopez, J., Liu, J., Kowar, C., Kapathy, S., Kally, S., Khan, Z., King, L., Li, Z., Liu, J., Loudon, P., Martin, R., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, S., Lopez, J., Martine, M., Marker, J., Loudon, P., Martine, R., Martinez, S., Liu, J., Martine, M., Marker, M., Marker, M., Marker, M., Marker, M., Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus clone CH230-248K16, ***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC118859.4 GI:23908219
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64734. .66070
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171951. .172050
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272055 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA linear HTG 12-OCT-2002
16, *** SEQUENCING IN PROGRESS
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Submitted (12-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 12, 2002 this sequence version replaced gi:21747309.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,B., Pul,-L., Puzzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sned,A., Sodergren,B., Song,X.-Z., Sorelle,R., Sosa,J., Steimie,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Steimie,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldcon,L., Walker,B., Wang,J., Walton,R., Walker,B., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Wallison,R., Wilson,R., Weig,X., White,F., Willison,R., Wilcozyk,B., Wooden,H., Worley,K., Wright,D., Wright,D., Wright,D., Walker,B., Voon,V., Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 272055)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
[see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html].

NOTE: This is a "working draft" sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                    be preserved.
                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 197058 bases at least Q40
Consensus quality: 200471 bases at least Q30
Consensus quality: 202766 bases at least Q30
Estimated insert size: 195853; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
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   133 AGAGCAUACGCUAGGU 148
                                                                                            73 UUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUACGUCACAGG 132
                                                                                                                                                                                                                                    13 UCUUGCGCGAUAAAUGCUGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUA 72
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/db_xref="taxon:10116"
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247897: gap of unknown length
261437: contig of 13540 bp in length
261537: gap of unknown length
267069: contig of 5532 bp in length
267169: gap of unknown length
268553: contig of 1384 bp in length
268653: gap of unknown length
270058: contig of 1405 bp in length
270158: gap of unknown length
270158: gap of unknown length
270158: contig of 1897 bp in length
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Gaps

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REFERENCE AUTHORS TITLE

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| RESULT 11 RECORDING SECTION APPROACH A | Db 17840 AAACAAGAGGCATGGT 17855 |
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| APDOUBZOS O 067 APDOUBZOS O 068 APDOUBZOS O 069 APDOUBZOS O 069 APDOUBZOS O 070 APDOUBZOS O 071 APDOUBZOS O 072 APDOUBZOS O 073 APDOUBZOS O 074 APDOUBZOS O 075 APDOUBZOS O 076 APDOUBZOS O 07 | 9209_064 9209_065 9209_066 |
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47; Conservative
                       AACTAAAGCAATCATAAGAGATTATCCACCATGCACAAATAATTATCCTTAAATTGGA 73082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-MAY-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA On Mar 20, 2001 this sequence version replaced gi:10122028. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=30: an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. Within the assembly from 57011-57037 there are unresolved GC compressions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing,R.A., Frisch,D., Presting,G., Wood,T.C., Yu,Y., Soderlund,CKim,H., Rambo,T., Henry,D., Simmons,J., Thurmond,S.K. and Mao,L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-APR-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA 4 (bases 1 to 152423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-SEP-2000) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA 3 (bases 1 to 152423) Wing,R.A., Frisch,D., Presting,G., Wood,T., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Henry,D. and Simmons,J.
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Wing, R.A., Frisch, D., P
Henry, D. and Simmons, J.
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Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa, complete sequence.
AC079853
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Kim,H.-R., Rambo,T., Henry,D. and Simmons,J.
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                                                                                                                                                                                                                                                                   repeat_region
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ASSSTLRLSSWQWCSRAPRRTWRAPYRIFSLETSLGPEFECMG"
                                                                                                                                                                                                                                                                        31743. .31879
                                                                                                                                                                                                                                                                                                                                                                       30319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPKRTTLKMDDTGAEEEVGDGVSEDASASEEEEEEEDDDDVVEEEEEEGAGLEGEWMPS
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PEPSTAGSTYATYLTELAESNAPAFLSHYYNIYFAHTTGGVAIGNKISKKILEGRELE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Inknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Similar to Explorer_Os1 MITE-like element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Similar to Stowaway01 type MITE element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="OSJNBb0004M10.3"
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|protein_id="AAK52553.1
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                                                                                                                                                                                                                                                                                                                                      imilar to Wanderer_Osl MITE element"
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                                                                                                                     969. .34140,34322. .34475,34553. .3
.35208,35303. .35535,35831. .36053)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Putative calmodulin-like protein"
/protein_id="AAK52557.1"
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LPAEAAASRIVKESVSSKGLRDDTTCIVVDILPPEKLSPPLKKHGKGGIKALFRRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="OSJNBb0004M10.
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                                  note="Similar to Tourist03 type MITE element"
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140405 AACTAAAGCAATCATAAGAGATTATCCACCATGCACAAATAATTATCCTTAAATTGGA 140348 ACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCCACAAAA 114 GUCUAGAUACGUCACAGGAGAGCAUACGCUAGGUCGCGUUGACUAUCCUUAUAUAUGA 172 Conservative 19.9%; Score 34.8; DB 15; 39.8%; Pred. No. 1.1; 19; Mismatches 52; Length 152423; 0 Gaps 0

.50877)

VERSION KEYWORDS SOURCE

HTGS_PHASE1

ORGANISM

Danio rerio

ACCESSION

unordered pieces.

REFERENCE

AUTHORS TITLE

Submission

JOURNAL

COMMENT

Web site:

LOCUS DEFINITION

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Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 9, 2004 this sequence version replaced gi:46194605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 55153; sum-of-contigs
Insert size: 204668; 10.0% error; agarose-fp
Quality coverage: 1.84x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 44793 bases at least (
Consensus quality: 48234 bases at least (
Consensus quality: 51319 bases at least (
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Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 57053)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: zC214B17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-APR-2004) Wellcome Trust Sanger Institute, Hinxton,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soon as it is available and the accession number will
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38388:
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/mol_type="genomic DNA"
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43692: contig of 2979 bp ii
43792: gap of 100 bp
46468: contig of 2676 bp ii
4658: gap of 100 bp
49179: contig of 2611 bp ii
49279: gap of 100 bp
51825: contig of 52546 bp ii
51925: gap of 100 bp
51925: contig of 5128 bp ii
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                                                                                                                                                                                             Score 34.4;
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114819
                                                        109
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                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Any regions longer than 1kb tagged as misc-feature 'unsure' are part of a tandem repeat of more than 10kb in length where it has not been possible to anchor the base differences between repeat copies. The region has been built up based on the repeat element to match the total size of repeat indicated by restriction digest, but tagged as misc-feature of the more digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: RMBL Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP database can be found at the MORMPEP clone-derived Caberafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              but repeat copies may not be in the correct order and the usual finishing criteria may not apply.

Location/Qualifiers
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DKEY-1101 is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute Center code: SC
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Submitted (17-JUN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests:
thtp://www.sanger.ac.uk/Projects/D rerio/faqs.shtml#dataeight
On Jun 17, 2005 this sequence version replaced gi:60417600.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 151303)
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                                                                                                                                                                AUUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCC 108
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                                                  ACAAAAGUCUAGAUACGUCACAGGAGAGCAUACGCUAGGUCGCGUUGA 156
                                                                                                              Conservative
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/clone_lib="DanioKey"
                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:7955"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Danio rerio"
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; Pred. No. 1.5;
16; Mismatches
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Sequence split into 5
Fragment Name
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BA00027-2
BA00027-3
BA000027-3
BA000027-4
Continuation T5 of 5)
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                                                                                                                                                                                                   13192 TCTAGCTGGTGAAGAGCTAACGTCACAGAGTTCTGTTGTTCTAATGGAGTTGGTGCAA 13133
13132 TACATCTTTTGACCACTAGATGGACTCGTGGATCACAGAAAAG 13090
                                                                                                                                                                                                                                                                                                         13 ИСПЛЕСССОМИАЛАМИ СОВОТОВНАТИ В ПОТОТОВНЕТВИТЕЛЬНИКИ В ПОТОТОВНЕТВИТЕЛЬНИТЕЛЬНИКИ В ПОТОТОВНЕТВИТЕЛЬНИКИ В ПОТОТОВНЕТВИТЕЛЬНИКИ В ПОТОТОВНЕТВИТЕЛЬНИКИ В ПОТОТОВНЕТВИТЕЛЬНИКИ В ПОТОТОВНЕТВИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬНИТЕЛЬН
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Similarity 40.8%; Pred. No. 1.7;
42; Conservative 18; Mismatches 43;
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Maximum Match 100%
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175
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4611.840 Million cell updates/sec
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Compugen Ltd.
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 19 | 18 | 17 | 16 | 15 | 14 | c 13 | 12 | 11 | 10 | 9 | ი 8 | c 7 | 6 | ຫ | 4 | w | N | _ | Result No. | |
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| 29.2 | 29.4 | 29.4 | 30.2 | 30.2 | 30.2 | 30.6 | 30.6 | 30.6 | 31.2 | 31.2 | 31.4 | 31.6 | 33.6 | 33.6 | 33.6 | 35.2 | 175 | 175 | Score | |
| 16.7 | 16.8 | 16.8 | 17.3 | 17.3 | 17.3 | 17.5 | 17.5 | 17.5 | 17.8 | 17.8 | 17.9 | 18.1 | 19.2 | 19.2 | 19.2 | 20.1 | 100.0 | 100.0 | Query | * |
| 1329 | 149062 | 129297 | 58000 | 200 | 188 | 22188 | 2022 | 1992 | 201 | 189 | 2398 | 5853 | 7442 | 5442 | 5355 | 9829 | 187 | 175 | Length | |
| 4. | 13 | 14 | 14 | σ | 8 | 4 | 9 | 8 | 6 | 8 | u | σ | 13 | 13 | 13 | 8 | 6 | 8 | 80 | |
| AAS51326 | ABD32608 | AEA61179 | ADZ42284 | AAL50547 | ABZ80710 | ABL28616 | ADA30421 | ACA21093 | AAL50546 | ABZ80709 | AAS72193 | ABA03158 | ADR84607 | ADR85194 | ADR85781 | AAL60324 | AAL50550 | ABZ80713 | ID | |
| Aas51326 Enterococ | Abd32608 Human can | Aea61179 Human FBR | Adz42284 Human Klo | Aals0547 Cricket p | Abz80710 Cricket p | Abl28616 Drosophil | Ada30421 DNA encod | Aca21093 Prokaryot | Aal50546 Drosophil | Abz80709 Drosophil | Aas72193 DNA encod | Aba03158 Streptoco | Adr84607 Aspergill | Adr85194 Aspergill | Adr85781 Aspergill | Aal60324 Aphid let | Aal50550 Rhopalosi | Abz80713 Rhopalosi | Description | |

The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation activity and function promotion, for producing useful proteins.

Claim 1; Page 34; 39pp; Japanese.

Nakashima N,

Shibuya N,

Nishikawa S;

(NAAG-) NAT INST AGROBIOLOGICAL SCI. (WAKE-) WAKENYAKU KK.

WPI; 2003-403230/38.

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| 27.8 | 27.0 | 2 2 8 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28 | 28.2 | 28.4 | 28.4 | 28.4 | 28.4 | 28.4 | 28.4 | 28.4 | 28.4 | 28.6 | 28.6 | 29 | 29.2 |
| 15.9 | 10.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.0 | 16.1 | 16.2 | 16.2 | 16.2 | 16.2 | 16.2 | 16.2 | 16.2 | 16.2 | 16.3 | 16.3 | 16.6 | TO. / |
| 119211 | 11000 | 32145 | 32145 | 9822 | 2458 | 1980 | 1261 | 882 | 882 | 882 | 820 | 147419 | 22080 | 2003 | 2001 | 1710 | 688 | 630 | 198 | 186 | 110000 | 383 | 1905 | 17.67 |
| 40 | ٥ ١ | 4. | .4 | ø | 9 | 11 | ω | 12 | œ | 0 | 9 | σ | N | w | ω | w | 13 | 13 | σ | œ | 14 | 0 | 12 | |
| AAF28553 | ADNOO49/ | ABL97544 | AAL04631 | ADB84054 | ADB84032 | ADM83140 | AAC36578 | ADN74128 | ADA67835 | ABZ13480 | ADB84055 | ABK83574 | AAX06751 | AAC49841 | AAC36174 | AAC43403 | ACN62473 | ACN54089 | AAL50548 | ABZ80711 | ADZ42285_1 | ABQ85268 | ADP98598 | MADDITOCHAN |
| Aaf28553 Genomic f | Continuation (18 o | Ab197544 Human tes | | | Adb84032 Murine NU | Adm83140 Rat vesic | Aac36578 Arabidops | Adn74128 Thale cre | Ada67835 Arabidops | Abz13480 Arabidops | Adb84055 Murine NU | Abk83574 Human cDN | Aax06751 Salmonel | Aac49841 Arabidops | Aac36174 Arabidops | Aac43403 Arabidops | Acn62473 Cotton de | Acn54089 Cotton an | Aal50548 Triatoma | Abz80711 Triatoma | Continuation (2 of | Abq85268 Arabidops | Adp98598 C. albica | MODULE OF PRICE COLOCOL |

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2001; 2001JP-00319923.
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wheatgerm; IGR-IRES;

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                              The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Rhopalosiphum padi virus RNA sequence of the invention
                                                                                                                                                                                                                   Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                       Claim 1; Fig 1-2; 38pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2001; 2001WO-JP000641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200261080-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhopalosiphum padi virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Rhopalosiphum virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                    WPI; 2002-627482/67
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Pred. No. 1.6e-53
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                                                                                                                                    paralysis virus). ALPV RNA is useful for controlling homopterous insects such as aphids or white files. It is useful in the research concerning aphids and for controlling aphids and in the field of agriculture or floriculture. It is also useful for detecting ALPV- viruses using PCR and for preparing a monoclonal antibody against antigen which is synthesised in vitro. The invention is also useful in gene therapy. The nrasent sequence is ALPV RNA
                                                                                                                      Sequence 9829 BP; 3083 A; 1906 C; 1879 G; 0 T; 2961 U; 0 Other
                                                                                                                                                                                                                                                        Claim 1; Page 10-13; 17pp; English.
                                                                                                                                                                                                                                                                                             Novel nucleic acid derived from aphid lethal paralysis virus, useful detecting ALPV-viruses, for preparing a monoclonal antibody against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aphid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aphid lethal paralysis virus
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                                               GGUUAGCUAUUUAGCUUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lethal paralysis virus; efly; agriculture; gene
                                                                                                                                                                                                                                                                                                                                                                                                         2001NL-01019225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  paralysis virus (ALPV)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods and compositions of the present invention are useful for diagnosing and/or treating invasive Aspergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be used in various drug discovery purposes, such as expression of the recombinant protein, hybridization assay and construction of nucleic acid arrays. The present sequence represents an Aspergillus fumigatus essential gene open reading frame, used during diagnosis and drug development in the invention. These genes share a high degree of sequence conservation with known essential genes of candida albicans. The sequence data for this patent is not represented in the printed specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invasive fungal infections, such as Farmer's lung disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 2418; 164pp; English.
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13-JUN-2003; 2003US-0478196P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained in electronic format from WIPO.
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ELITRA CANADA LTD.
                                                                                                                                                                                                                                                                                            5355 BP; 1369 A; 1314 C; 1377 G; 1295 T; 0 U; 0 Other;
                                                                                                                                                                                        UGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCCACAAAAGUCUAGAU 122
                                                                                                                                                                                                                                                           TCTTCTGAGGGCAGACCGGATAATGGCCGATGTCACAGCATTGGAAACAACCGAACCACT 3008
                                                            ACGUCACAGGAGAGCAUACGCUAG 146
                                                                                                                        TCCTCTACAGTCTACCATTTCTGAGCTGGAAGATGGAATGGACAAACTAAAAATTCGGGG 3068
AAGTAGCAGGAGAGCACAACCAAG 3092
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Pred. No. 0.29;
L9; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invasive fungal infections, such as Farmer's lung disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 1418; 164pp; English.
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13-JUN-2003; 2003US-0478196P
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drug screening; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-2004
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ELITRA CANADA LTD.
                                                                                                                                                                                                                                                                                                                                                                                        h 19.2%; Score 33.6; DB Similarity 38.9%; Pred. No. 0.29; S6; Conservative 19; Mismatches
                                                                                                                                                                                       UGGUUAGCUAUUUAGCUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAU 122
                                                                                                                             TCCTCTACAGTCTACCATTTCTGAGCTGGAAGATGGAATGGACAAACTAAAAATTCGGGG 3068
   AAGTAGCAGGAGAGCACAACCAAG
                                                                ACGUCACAGGAGAGCAUACGCUAG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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   3092
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RESULT 6

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         ABA03158 standard; DNA; 5853
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13-JUN-2003; 2003US-0478196P.
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ELITRA CANADA LTD.
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                                                                                                                                                                                                                          ACGUCACAGGAGAGCAUACGCUAG 146
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13-FEB-2002

(first entry)

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Best Local &
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Mengaud J,
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                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCTCAAGTGCCGAACGAAGTTCTGGCGCAAAAATAACGACTGCTGCAATAGCACCATA 378
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

WO200175067-A2

DNA encoding novel human diagnostic protein #7997.

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                                                                                                                                                                                                                                                                                                                                                      CC sequences. (I) is useful as hybridisation probes, polymerase chain Creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC extivity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC involving aberrant protein expression or biological activity. The CC involving aberrant protein expression or biological activity. The CC disgnostics, gene mapping, identification of mutations CC disgnostics, gene mapping, identification of mutations CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS44197-AAS94564 represent novel human diagnostic CC coding sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC fraction format directly from WIPO at
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                        Sequence 2398 BP; 561 A; 563 C; 611 G; 663 T; 0 U; 0 Other;
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23-AUG-2000; 2000US-00649167.
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GTCTGTAGTTCGGGAGTTTCCGTTA 1530
                                                                             CUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAG 120
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                                       AUACGUCACAGGAGAGCAUACGCUA 145
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ilarity 37.2%;
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AAL50546;

AAL50546 standard; RNA; 201 BP

Drosophila C virus RNA sequence.

(first

CrPV-like virus; ss; higher-order structure; drug development; drug production; translational activity-promoting function;

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RESULT 10 AAL50546

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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to to a cell-free protein synthesis system derived from wheatgerm where there is substantial exclusion of wheatgerm embryo albumen impurities. The novel system uses a sequence having a higher-order RNA structure that promotes translation activity. The higher-order sequence is preferably a "pseudoknot", especially derived from a range of viruses (ABZ80707-ABZ80713). This sequence represents the "pseudoknot" higher-order sequence from the Drosophila C virus. The sequence is used in a construct which may also include an intergenic region and internal ribosome entry site (IGR-IRES). The method is applicable in producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translactivity and function promotion, for producing useful proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NAAG-)
(WAKE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudoknot; secondary structure; cell-free protein synthesis; albumen; impurity; higher-order structure; intergenic region;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 189 BP; 57 A; 30 C; 34 G; 0 T; 68 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 32; 39pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-403230/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2001; 2001JP-00319923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-2002; 2002WO-JP010447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003033719-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila C virus derived pseudoknot sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ80709 standard; RNA; 189
                                                                                                                                                                                                                                                                                                     Local
                                                               113
                                                                                                                                  65
                                                                                                                                                                                               53 СИАСААСАСИИ СБИЙА СИЛИМИ В СИМИНА СИЛАНИ СА В СОВЕТИ В СИМЕДЕ В СИМЕДА С СОВЕТИ В С
                                                                                                                                                                                                                                                                                                  17.8%;
Similarity 66.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAT INST AGROBIOLOGICAL SCI WAKENYAKU KK.
                                                            AAGUCUAG 120
                                                                                                                               CUUAAUAAUUAGGUUAACUAUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUA 124
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              z,
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                                                                                                                                                                                                                                                                  Score 31.2; DB Pred. No. 0.62; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                     Length 189;
                                                                                                                                                                                                                                                                     Indels
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protein synthesis; structural analysis

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Best Local :
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21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises seven RNA sequences (CrPV-like viruses) which have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Drosophila C virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in springers of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-627482/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001; 2001JP-00016746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2001; 2001WO-JP000641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila C virus
                                                   21-MAR-2002;
                                                                            03-OCT-2002
                                                                                                                             Acinetobacter baumannii
                                                                                                                                                                 Antisense; ds; prokaryotic essential gene;
                                                                                                                                                                                                                   19-JUN-2003
                                                                                                                                                                                                                                                                    ACA21093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NAAG-) NAT INST AGROBIOLOGICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200261080-A1
                                                                                                   WO200277183-A2
                                                                                                                                                                                        Prokaryotic essential gene #2750
                                                                                                                                                     design;
                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                  standard; DNA; 1992 BP
                                                                                                                                                                                                                                                                                                                                                                                                  CUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGGGCAGCCCACAA 112
                                                                                                                                                                                                                                                                                                                                  AUAUCCAG 132
                                                                                                                                                                                                                                                                                                                                                         AAGUCUAG 120
                                                                                                                                                                                                                                                                                                                                                                                  CUUAAUAAUUAGGUUAACUAUUUUAGUUUUACUGUUCAGGAUGCCUAUUGGCAGCCCCAUA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
2001US-00815242.
2001US-00948993.
2001US-0342923P.
                                                   2002WO-US009107.
                                                                                                                                                     gene.
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kanamori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 A; 33 C; 35 G; 0 T; 72 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31.2; DI
Pred. No. 0.64
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                  cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ADA30421
ID ADA
XX
AC ADA
XX
AC ADA
XX
XX
DT 20-XX
DE DNA

20-NOV-2003 ADA30421;

(first entry)

DNA encoding Acinetobacter baumannii protein #1708

RESULT 12

ADA30421 standard; DNA;

2022

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CC the 6213 antisense sequences given in the specification where expression could be acted inhibits proliferation of a cell. Also included are:

((1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense could concleic acid; (4) a host cell containing the vector; (3) an isolated controlled acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the cantisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an compound which the test compound that inhibits proliferation of an compound acts; (9) manufacturing an antibiotic; (10) profiling a compound source of the strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of collection of an organism. The antisense nucleic acids are useful for identifying proliferation to isolate candidate molecules for rational cross of collection of collection of an organism. The antisense nucleic acids are useful for required for proliferation in cells other than S. aureus, S. typhimurium, the properation of the target for this narent did antisense organism for the acrusing the terrains for this narent did antisense organism for the carget of a compound that inhibits the confidence of a compound that inhibits the confidence of the carget of a compound that inhibits the confidence of the carget of a compound that inhibits the confidence of the carget of a confidence of the carget of a confidence of the carget of a confidence of the carget of a confidenc
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                                                                                                                                                                                     Matches
                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                         Sequence 1992 BP; 639 A; 402 C; 410 G; 541 T;
                                                                                                                                                                                                                                                                                                                                          K. pneumoniae or P. aeruginosa. The present sequence is one of the target
prokaryotic essential genes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 8963; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-)
                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-029926/02.
DB; ABU17223.
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                                                                                                                                      30 ИСАССИСАЛАЛАССИИСССИЛИИССИАСЛАСАСИИССИИЛАСИЛИИЛАСИИИЛАСИЛИЛИСА 89
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                                                                                                                                                                                                           Similarity
                                                                                      Zamudio C,
Trawick JD,
  TGATGGCGCAGATCATGCGAAACAA 816
                                             AGACGCCGUCGUGCAGCCCACAAAA 114
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malone
Carr G
                                                                                                                                                                                                      17.5%; Score 30.6; D
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                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                              DB 8;
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Forsyth
                                                                                                                                                                                        34;
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                                                                                                                                                                                                                              Length 1992;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                0 Other;
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Xu HH;
                                                                                                                                                                                        0
                                                                                                                                                                                     Gaps
                                                                                                  791
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Fri

Dec

23 12:17:51 2005

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vaccine;
                                                                                        gene; Acinetobacter baumannii; bacterial disease; antibacterial;
cine; plant biocontrol agent.
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09-JUN-1998; 04-JUN-1999; 13-MAY-2003 Acinetobacter baumannii. US6562958-B1 98US-0088701P. 9905-00328352

(GENO-) GENOME THERAPEUTICS CORP.

WPI; 2003-576092/54. Breton ຸດ Bush D;

P-PSDB; ADA34547.

New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for

Example; SEQ ID NO 1708; 328pp; English

The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii invention relates to isolated Acinetobacter baumannii nucleic acids

> 105 19508

0

Sequence 2022 BP; 648 A; 407 C; 410 G; 557 T; 0 U; 0 Other;

Query Match Best Local S Matches 38 38; Similarity Conservative 17.5%; 44.7%; ; Pred. No. 2.5; 13; Mismatches Score 30.6; Pred. No. 2 DB 9; 34; Length 2022; Indels <u>,</u> Gaps

밁 ঠ 759 30 TAATATGCAAACGGTCCAAATTGCTAAAAAGCTTGGTATGCCAATTACCATCACGCTTGA UGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCA 89 818

용 Ś 819 90 AGACGCCGUCGUGCAGCCCCACAAAA 114 TGATGGCGCAGATCATGCGAAACAA 843

RESULT 13
ABL28616/c
ID ABL286
XX ABL286
XX ABL286
XX Drosop
XX Drosop
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XX Drosop ABL28616 standard; DNA; 22188 ВP

26-MAR-2002 ABL28616 (first entry)

melanogaster genomic polynucleotide SEQ ID NO 37321.

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.

Drosophila melanogaster

WO200171042-A2

27-SEP-2001

23-MAR-2001; 2001WO-US009231.

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                                                                  В
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                                                                                                                                   Matches
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL3051), expressed DNA sequences (ABL0175) and the encoded proteins (ABB57737-babB72072). The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 37321; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                    Sequence 22188 BP; 6664 A; 5376 C; 4559 G; 5589 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
                                                                                                                                                    Local
 19507
                                 106
                                                                                                  46
                                                                                                                                   39;
                                                                                                                                                    Similarity
                                                                CGTAAATGAACCATAATTGGATCGCTATATAGATTTTTTATTCGATGGTGATGCCTCAGG
                                                                                                  CGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAG
                               CCCACAAAAGUCUAGAUACGUCACAGGAGAGCAUACGCUAG 146
CTTAGATCTGTTTTCGTAAGTGGAAGCAGAGCATACGCGAG
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                                                                                                                                   Conservative
                                                                                                                                                   17.5%;
38.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                   18; Mismatches
                                                                                                                                                   Score 30.6; DI
Pred. No. 6.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                  DB 4;
                                                                                                                                   44;
                                                                                                                                                                  Length 22188;
                                                                                                                                   Indels
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RESULT 14
ABZ80710
ID ABZ80
XX ABZ80
XX DF Cric)
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XX WO20
XX WO30
XX WO30
XX I7-C
XX INAL
XX NAL
XX NAL
XX WPI
XX WPI
XX WPI Cricket paralysis virus derived pseudoknot sequence. 15-OCT-2003 ABZ80710; ABZ80710 standard; RNA; 188 BP (first entry)

Pseudoknot; secondary structure; cell-free albumen; impurity; higher-order structure; internal ribosome entry site; ss. protein synthesis; intergenic region;

Cricket paralysis virus.

WO2003033719-A1

08-OCT-2002; 2002WO-JP010447

17-OCT-2001; 2001JP-00319923

NAT INST AGROBIOLOGICAL WAKENYAKU KK. SCI

Nakashima N, Shibuya N, Nishikawa

WPI; 2003-403230/38

Cell-free protein synthesis means in wheatgerm system to establish overexpression of target gene with base sequence sustaining translation

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RESULT 15
AAL50547
ID AAL50
XX ALSO
XX 19-DE
XX Crick
XX Crpv-
KW drug
KW prote
XX M drug
KW DF 08-AU
XX 25-JJ
PR 31-JJ
XX 25-JJ
PR 11-JJ
XX WPI;
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           have a higher-order structure that sustains translational activity-promoting function. The RNA sequences of the invention are useful in the synthesis of proteins and polypeptides for application in developing and producing drugs. The RNA sequences of the invention are also useful in basic research of protein synthesis and structural analysis by the gene recombinant technique. The present nucleotide represents a Cricket paralysis virus RNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CrPV-like virus; 88; higher-order structure; drug drug production; translational activity-promoting protein synthesis; structural analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 188 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 33; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational activity-promoting higher-order structure of CrPV-like viruses for protein translation when suitably initiated, useful in synthesis of proteins and polypeptides of foreign species for application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-627482/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cricket paralysis virus RNA sequence
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                                                                                                                                                                                                                                                                                   The invention comprises seven RNA sequences (CrPV-like viruses) which
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1-2; 38pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakashima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001JP-00016746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41,
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ilarity 69.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kanamori Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 A; 33 C; 36 G; 0 T; 63 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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function;
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                                                                               Sequence 200
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                                                  Similarity
                UUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAAGUCUAG 120
UAGGUUAGCUAUUUAGCUUUACGUUCCAGGAUGCCUAGUGGCAGCCCCACAAUAUCCAG 131
                                        Conservative
                                                                               BP; 60
                                                                                 A; 36 C;
                                                17.3%;
                                       Score 30.2; DB Pred. No. 1.5; 0; Mismatches
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                                                                                 37 G;
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                                                                                  67 U; 0 Other;
                                                            DB 6;
                                         18;
                                                            Length 200;
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Search completed: December 22, Job time: 255.897 secs 2005, 08:40:43

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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                 seq length: 0
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DE054751 Oryzias 1

C0094958 GR Ea17F

CV549123 TGESTZYT3

DR948423 EST113996

CC9460819 720727 MA

CC093661 GR Ea15F

AJ819306 AJ81306

AJ812852 AJ813306

CC079367 GR Ea42B

AJ812852 AJ816139

CC079367 GR Ea40J

CC079363 GR Ea40J

CC079363 GR Ea30M

CC071935 GR Ea30M

CC071935 GR Ea30M

CC073836 GR Ea30M

CC073836 GR Ea30M

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| 30.2 | 30.2 | 30.2 | 30.4 | 30.4 | 30.4 | 30.6 | 30.6 | 30.6 | 30.6 | 30.6 | 30.6 | 30.6 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 30.8 | 31 | 31.2 | 31.2 | 31.2 |
| 17.3 | 17.3 | 17.3 | 17.4 | 17.4 | 17.4 | 17.5 | 17.5 | | | | | 17.5 | | 17.6 | 17.6 | | | | 17.7 | | | 17.8 |
| 546 | 513 | 506 | 796 | 677 | 633 | 706 | 679 | 539 | 490 | 486 | 433 | 367 | 771 | 764 | 753 | 436 | 432 | 355 | 797 | 886 | 704 | 664 |
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| AQ619135 | BI725906 | BI725753 | CO474911 | CO231499 | ВН199599 | DR021893 | CL555745 | CO337794 | CO153765 | CO153454 | C0153155 | BW873346 | CZ132703 | CG817558 | CZ576752 | BP649595 | AV787699 | DN466392 | AG290940 | AG877925 | CR342428 | AV275598 |
| AQ619135 HS_5173_B | BI725906 1031081H0 | BI725753 1031081A0 | CO474911 GQ0068.TB | CO231499 WS0051.B2 | BH199599 Sm1-45G9. | DR021893 STRS1_47_ | CL555745 OB_Ba000 | CO337794 EN15317.5 | CO153765 EN02756.5 | CO153454 EN02010.5 | CO153155 EN01401.5 | BW873346 BW873346 | CZ132703 OA_BBa002 | CG817558 SOYAL37TV | CZ576752 OA_BBa017 | BP649595 BP649595 | AV787699 AV787699 | DN466392 USDA-FP_1 | AG290940 Mus muscu | AG877925 Oryza sat | CR342428 mte1-75M5 | AV275598 AV275598 |

RESULT 1 CO224988/c LOCUS DEFINITION

ALIGNMENTS

| JOURNAL (| TITLE 1 | (n > | · | AUTHORS F | REFERENCE 1 | re. | hr | ORGANISM E | SOURCE E | KEYWORDS E | VERSION C | ACCESSION C | ~ | DEFINITION W | Locus |
|--------------------|--|---|---|---|------------------|---|--|------------------|---------------------------------|------------|------------------------|-------------|--------------------------------|--------------|---|
| Unpublished (2005) | Ritland, K. and Bohlmann, J. The spruce transcriptome: Analysis of expressed sequence tags from The spruce transcriptome: Analysis of expressed sequence tags from | Mayo,M., Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritland,C.E., Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., | <pre>Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G., Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,</pre> | Ralph, S., Kolosova, N., Oddy, C., Cooper, D., Butterfield, Y., | (bases 1 to 448) | Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | Picea sitchensis | Picea sitchensis (Sitka spruce) | ST. | CO224988.1 GI:49047303 | CO224988 | WS01026_D16 3', mRNA sequence. | cea sitche | CO224988 448 bp mRNA linear EST 22-JUN-2004 |

| Unpublished (2005) Contact: Joerg Bohlmann Cenome BC forest genomics program University of British Columbia Michael Smith Laboratories, 6174 University Boulevard, Vancouver, British Columbia, Canada, V6T 1Z3 Tel: 1-604-822-0282 Fax: 1-604-822-2114 Email: bohlmann@msl.ubc.ca Plate: W501026 row: D column: 16 High quality sequence stop: 448 POLYA=Yes. | | | | | | | | | | | COMMENT | JOURNAL | |
|--|------------|---------------------------------|----------------------------------|----------------------------|---------------------|---------------------|--|--|--------------------------------|-----------------------------------|-------------------------|--------------------|--|
| | POLYA=Yes. | High quality sequence stop: 448 | Plate: WS01026 row: D column: 16 | Email: bohlmann@msl.ubc.ca | Fax: 1-604-822-2114 | Tel: 1-604-822-0282 | Vancouver, British Columbia, Canada, V6T 123 | Michael Smith Laboratories, 6174 University Boulevard, | University of British Columbia | Genome BC forest genomics program | Contact: Joerg Bohlmann | Unpublished (2005) | |

FEATURES source /db xref="taxon:3332"
/clone="WS01026_D16"
/clone="WS01026_D16"
/sex="Hermaphrodite"
/tissue_type="Young root growth (terminal 1-3 cm) and old root growth (distal to terminal 1-3 cm) tissues"
/dev_stage="three year old clonal trees grown under greenhouse conditions in standard potting soil mixture." Location/Qualifiers /organism="Picea sitchensis" /mol_type="mRNA" /cultivar="Gb2-229"

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REFERENCE
AUTHORS
TITLE
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CG949276/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Town,C.D., Shetty,J., I
Sequencing of BAC ends
Unpublished (2003)
Other_GSSs: MBEAR58TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBEAR58TF mth2 Medicago truncatula
                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
Seq primer: TGTAAAACGACGGCCAGT
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG949276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CG949276.1 GI:39858599
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                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 835)
                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Drive, 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli DH10B cells"
/(clome lib="SS-R-N-A-11"
//clome lib="SS-R-N-A-11"
//note="Organ: Roots; Vector: pBluescript II SK (+) XR;
/note="Organ: Roots; Vector: pBluescript II SK (+) XR;
/site_1: EcoRI (5' end of cDNA); Site_2: XhoI (3' end of cDNA); mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6 (9):791] in order to reduce the abundance of highly expressed transcripts."
                                                                                                                                                          /organism="Medicago truncatula"
/mol type="genomic DNA"
/cultivar="genotype A17"
/db xref="#taxon:3880"
/clone="15120"
                                                                                         /clone_lib="mth2"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Cook, D.R. and Kim, D.J, unpublished"
                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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  20.6%;
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51.6%; Pred. No. 0.066;
tive 15; Mismatches 16;
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  Score 36; DB 1
Pred. No. 0.49;
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Medicago truncatula
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AIAA-aaf34c01.bl Ancylostoma caninum whole genome shotgun library sequence.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 494)
Mitrova,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,RRonko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R.
Genome Survey sequences from the parasitic nematode Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Mitreva M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ancylostoma caninum (dog hookworm)
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CZ209094.1 GI:59212993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequenced by Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic DNA provided by John Hawdon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: nematode@watson.wustl.edu
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AGGTCGAGGTAACAACAATTCAGATTATCCACATGTGTGGTTTCAAGAGCTAG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pOTW13; Site 1: BstX1; Site 2: BstX1; Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjmh@gwunc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."
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library (AIAAGSS 001)"
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/lab_host="GS10"
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E-mail: htakeda.s.u-tokyo.ac.jp
(2) Department of Biological Science,
University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-003
Phone: +81-3-5841-4431
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(1) Department of Biological Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-003
Phone: +81-3-5841-4431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045 (B-mail:afujiyam@ggc.riken.jp, URL:http://stt.gsc.riken.jp/, Tel:81-3-4212-2558, Fax:81-3-3556-1916)
This work was done in collaboration with Takeda, H. (1), Narr (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2005) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pujiyama,A., Toyoda,A., Kuroki,Y. and Sakaki,Y. BAC end sequences of Olal Oryzias latipes Library Published Only in Database (2005) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
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Oryzias latipes DNA, clone: ola1-025E15.F, genomic survey sequence
DE054751
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(3) Department of Biological Science,
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Oryzias latipes
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Phone: +81-3-5841-4431
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ucuugcgcgauaaaugcugacgugaaaacguugcguauugcuacaacacuugguuagcua 72
                                                              TCTAGCTGAAGAGCTAACGTCACAGAGTTCTGTTGTTCTAATGGAGTTGGTGTGCAA
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ite 1 : SacI
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Location/Qualifiers
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library"
                                                                                                                                                                                                                                                                                                                  /organism="Oryzias latipes"
/mol_type="genomic DNA"
/db_xref="taxon:8090"
/clone="0181-025E15.F"
                                                                                                                                                                                                                                                                                                 sex="male"
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|-|lib="BAC end sequences of Olal Oryzias latipes
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GR__Ea171
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TgESTZyr32b05.y3 Tg COUG Tachyzoite cDNA Library Toxoplasma CDNA Clone TgESTZyr32b05.y3 5', mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
Tang, K.,
                 Sarcocystidae; Toxoplasma.

1 (bases 1 to 588)
                                                    Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia;
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CV549123.1
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Location/Qualifiers
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Kim,H., Yu,Y., Kudrna,D.,
Udail,J.A., Rapp,R.A., We
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CO094958
CO094958.1 GI:48793644
                                                                                     Toxoplasma
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Fax: 520 621 1259
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The University of Arizona Forbes Building Room 303,
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   Cole, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GR_Ba" | Sa" | Site_1: NotI; Site_2: /note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2: EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-FV. Colonies plated/picked by AGI. More glycerol clones held in -80."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db xrer= "colore" (R__Ba17F18"
/clone="GR__Ba17F18"
/tissue_type="whole seedlings"
/tissue_type="whole seedlings"
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lab_host="DH10B"
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db_xref="taxon:29730"
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                                                                                     gondii
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41.9%; Pred. No. 2.7;
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   Fogarty, S.,
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cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 744;
     Ajioka, J.A., White, M.,
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                     Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mueller,C.,
erlund,C. and
                                                                                                                                                                                      EST 22-OCT-2004
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GR_Ea17F18 5',
                                                                                                                                                                                                                                                                                                                                                                                                        <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                      gondii
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RESULT 7
DR948423
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     TITLE
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                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 GAUCUUGCGCGAUAAAUGCUGACGUGAAAAACGUUGCGUAUUGCUACAACACUUGGUUAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R. Toxoplasma EST Project Unpublished (2001)
Contact: Clifton, S. Toxoplasma EST Project Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                          Aquilegia formosa x Aquilegia pubescens Aquilegia formosa x Aquilegia pubescens Eukaryota; Viridiplantae; Streptophyta; Embryo Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculaceae; Aquilegia.

1 (bases 1 to 856)
                                                                                                                                                                                                                                                                                                                     DR948423
856 bp mRNA linear EST1139962 Aquilegia cDNA library Aquilegia formosa pubescens cDNA clone CO1RB13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: T7 from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: toxo@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Hodges,S.A., Rensink,W., Buell,C.R., Nordborg,M. and Tomkins,J.
Generation of ESTs from Aquilegia
                                                                                                                                                                                                                                                                       DR948423.1 GI:71717786
                                                                                                                                                                                                                                                                                                DR948423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTGÁGCAACAAGAAGGCGACGGGCGTCGGGCAACCAAAATGGGTTCGCATGCAGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUACGUCACA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCTGGGGTGACGAGTGCACTCTCGCTGTGATGGCGGAGATGTACAACATCCGGATCGT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTTATCATACCATACGATGTGGTTCCT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGAGCAUACGCUAGGUCGCGUUGACU 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 588.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db xref="taxon:5811"
/db xref="taxon:5811"
/clone="TgESTZy232055,y3"
/dev stage="Tachyzoite"
/lab host="GC10 Competent Cells(PGC)"
/lab host="GC10 Competent Cells(PGC)"
/clone lib="Tg COUG Tachyzoite cDNA Library"
/clone lib="Tg COUG Tachyzoite cDNA Library"
/clone lib-mrg COUG Tachyzoite dDN Keliang Tang, and Robert COLA library was constructed by Keliang Tang, and Robert COLA using the template-switching PCR method (Creator CDNA using the template-switching PCR method (Creator SMART cDNA, Clontech Inc.). First strand was PCR amplified using the same primer set and the fragments were digested with Sfil. The fragments were size selected, ligated into vector pDNR LIB containing directional Sfil sites, and electroporated into GC10 competent cells. WARNING: the library contains a small percentage of cDNAs derived from the human host cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                         Borevitz, J., Kramer, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
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                                                                                                                                                                 Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 588;
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                                                                                                                                                                                                                                                                                                                                                      x Aquilegia
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AUTHORS
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ORGANISM
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720727 MARC (
CB460819
CB460819.1 (
EST.
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Other ESTS: EST1139961
Contact: Scott Hodges
Contact: Scott Hodges
Department of Ecclogy, Evolution and Marine Biology
University of California, Santa Barbara
Santa Barbara, CA 93106, USA
Tel: 805 893 7813
Fax: 805 893 4724
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Seq primer: M13 Reverse.
                                       A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
                                                                                                        Pecora; Bovidae; Bovinae; Bo
1 (bases 1 to 717)
Smith, T.P.L., Roberts, A.J.,
Wray, J.E. and Keele, J.W.
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGATAATTGGATTTATTATTGGAGTCG
DA, ARS, US Meat Animal Research Center
Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   flower buds, leaves and roots"

/lab host="DH10B T1 (T1 and T5 phage resistance)"

/clone 11b="Aquilegia cDNA library"

/clone 11b="Aquilegia cDNA library"

/note="Vector: pCMV SPORT6.1; Site 1: EcoR1; Site 2: Not1;

F2, F3, and F4 lines of Aquilegia Formosa X A. pubescens were grown from seed in greenhouses at UC Santa Barbara.

From these plants three sets of tissue were collected: 1)

Small flower buds (<10 mm) and very young inflorescences (71 & 29% by weight respectively), 2) Medium (7-20 mm) and large (at or near anthesis) flower buds (65 & 35% by weight respectively) and 3) Shoot apical meristens. A fourth set of tissue was collected from plants of A. formosa. These plants were grown from seed in sand and at approximately 1 month root tissue and leaf tissue of various developmental stages were collected (84 & 16% by weight respectively). Total RNA was extracted from each set of tissue and pooled in the following proportions:

1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled total RNA, mank, was extracted and enriched for full-length messages and then normalized with proprietary methods by Invitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:338618"
/clone="CO1RB13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Aquilegia formosa x Aquilegia pubescens"
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                                                                                                                                                                                                                                                                  (cow)
                                                                                                                                                                                                                                                                                                            GI:29267203
                                                                                                                                                                                                                                                                                                                                                          6BOV Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %; Score 32.6; D
%; Pred. No. 7.2;
16; Mismatches
                                                                                                                                                                               вов.
                                                                                                                                                                                                                                                                                                                                                   7 bp mRNA linear cDNA 5', mRNA sequence.
                                                                                                                                   Echternkamp, S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              띪
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
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                                                                                                                                      Chitko-McKown, C.G.,
                                                                                                                                                                                                                                                                                                                                                                                    EST
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JOURNAL COMMENT
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CO093661
LOCUS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 GACGCCGUCGUGCAGCCCACAAAAGUCUAGAUACGUCACAGGAG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 GACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUUUACUAAUCAA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CO093661
GR__Ea15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium raimondii
Gossypium raimondii
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiglantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiglantae; eudicotyledons;
core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids []; Malvales; Malvaceae; Malvoideae; Gossypium.
[] (bases l to 760)
[] (bases l to 760)
Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
Wing, D., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C.
                                                                                                                                                                                                                                     Email: rwing@genome.arizona.edu
Plate: 15 row: F column: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Tel: 520 626 9595
Pax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                      Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called trimmed with the aid of the trim_alt cross_match v0.990329.
Plate: FQY8077 row: P column: 19
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Global assembly of Cotton ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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Fax: 402 762 4390
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Eal5F23.f GR__Ea Goвsypium raimondii cDNA clone GR__Eal5F23 5′,
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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
/clone="GR_Ea15F23"
/tlssue_type="whole seedlings"
/tlssue_type="first true leaves"
/dev_stage="first true leaves"
/lab host="UP10B"
/clone_lib="GR_Ea"
/clone_lib="GR_Ea"
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
                                                                                                                                           /organism="Gоввурium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
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Pred. No. 11;
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                                                                                    214 ATATAATGATGTGACTAACTTCTGTATTCTTCTGAAAAATGCATAACACTTTAGCCTTT
154 AGTTAGAAAGGAGCTGTCTGGTCACACTAACAATTTTACAGA 113
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                                       82 ACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
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AJ819306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
1:ECORV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
constructed from pooled monocytes from Bos taurus (Holstein) and
Bos indicus (Sahiwals) cattle subjected to various stimuli,
including infection with the protozoan parasite Theileria annulata.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The expanding role of microarrays in the investigation macrophage responses to pathogens vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
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1 (bases 1 to 776)
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                                                                                                                                                                                                                                                                                 /tissue_type="blood"
/cell type="blood"
/cell type="bovine monocyte"
/close lib="NO206"
/close lib="NO206"
/close lib="NO206"
/close lib="NO206"
/close lib="NO206"
/close lib="NO206"
/close lib-rary constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KN206 Bos sp. cDNA clone C0006014p06, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos sp."
/mol_type="mRNA"
/db_xref="taxon:29061"
/clone="C0006014p06"
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                                                                                                                                                                                               18.1%; Score 31.6; 36.3%; Pred. No. 16;
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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C0079367
C0079367.1 GI:48748848
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Global assembly of Cotton ESTs
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Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Udail,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
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                                                                                                                            вов вр.
  1 (bases 1 to 800)
McGuire, K. and Glass, E.J.
The expanding role of microarrays in the investigation of
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                               ACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
                                                                                                                                                                                                                                                                                                                                                      TCACATCCAAACATCGTCCCAAGCCTTCCAAATGCACAAATA 752
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42 row: B column: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="GR__Ea" | /clone_lib="GR__Ea" | /clone="Vector: pCMV.SPORT-6.1; Site_1: Not1; Site_2: /note="Vector: pCMV.SPORT-6.1; Site_1: Not1; Site_2: EcoRV; Library made by Invitrogen with RNA supplied by EcoRV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into Not1-EV. Colonies wendle lab. Directional cloned into Not1-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."
                                                                                                                                                                                                                                  KN206 Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="GR_Ea42B19"
/tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:29730"
                                                                                                                                                                                          GI:51880328
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                                                                                                                                                                                                                                sp. cDNA clone C0005205p20, mRNA sequence
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GR__Ea42B19 5',
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Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
1:ECORV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
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AJ816139 KN206 Bos sp. cDNA clone C0005202b20, mRNA sequence.
AJ816139
AJ816139.1 GI:51883615
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                                                                                                                                                 Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscol
v0.020425.c. Vector identified by cross match with the -minscol
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site
1:EcoRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
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The expanding role of microarrays in the investigation of macrophage responses to pathogens
vet. Immunol. Immunopathol. 105 (3-4), 259-275 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Boyidae; Boyinae; Bos.
                                            constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata.
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Genomics and Genetics
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Site_2: NotI; Normalised library constructed from pooled
monocytes from Bos taurus (Holstein) and Bos indicus
(Sahiwals) cattle subjected to various stimuli, including
infection with the protozoan parasite Theileria annulata"
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/cell_type="bovine monocyte"
/clone_lib="KN206"
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/mol type="mRNA"
/db_xref="taxon:29061"
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Gossypium raimondii
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@genome.arizona.edu
Plate: 40 row: J column: 04.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
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Fax: 520 621 1259
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/dev gtage="first true leaves"
/lab_nost="PH108"
/clone_lib="GR_Ea"
/clone_lib="GR_Ea"
/clone_lib="GMV.SPORT-6.1; Site_1: NotI; Site_2:
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
BCoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."
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/cell type="bovine monocyte"
/close lib="WAYO6"
/close lib="WAYO6"
/close lib="WAYO6"
/note="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
Site_2: NotI; Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gossypium raimondii"
|mol_type="mRNA"
|db_xref="taxon:29730"
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                                                                                                                                                                                                Best
                                                                                                                                                                                                                  Query Match
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                                        82 ACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
                                                                                                                          22 AUAAAUGCUGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUU 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 818)
1 (bases 1 to 818)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@genome.arizona.edu
Plate: 30 row: M column: 01.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Global assembly of Cotton ESTs Unpublished (2004)
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                               /clone lib="GR Ea"
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
ECORV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
                                                                                                                                                                                                                                                                               plated/picked by AGI. More glycerol clones held in -80.
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/dev_stage="first true leaves"
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/db_xref="taxon:29730"
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39.2%; Pred. No. 16;
tive 18; Mismatches
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prime.
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is derived by analysis of the total score distribution.
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4226.575 Million cell updates/sec
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Sequence 1334, A
Sequence 1708, Ap
Sequence 13089, A
Sequence 13539, A
Sequence 1830, A
Sequence 40, Appl
Sequence 144624,
Sequence 1149, Ap
Sequence 20259, Ap
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| 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.1 | 15.2 1 | | 15.2 | 15.2 | 15.2 | 15.2 |
| 7496 | 6387 | 6387 | 3466 | 2565 | 2553 | 2509 | 1655 | 1539 | 1539 | 1539 | 693 | 601 | 109 | 444 | 165651 | 154600 | 94987 | 2865 | 590 | 425 |
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| 16025, A | 1, Appli | 1, Appli | 10, Appl | 1052, Ap | 488, App | 4283, Ap | 4529, Ap | 7, Appli | 6, Appli | 5, Appli | 195, App | 152512, | 27382, A | 6916, Ap | 13032, A | 14757, A | 12510, A | 14817, A | 3654, Ap | 11107, A |

ALIGNMENTS

RESULT 1 US-09-270-767-1072

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; Sequence 1072, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1072
; LENGTH: 1345
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1072
                 Sequence 16354, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16354
LENGTH: 1345
TYPE: DNA
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ORGANISM: Drosophila melanogaster
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47.5%; Pred. No. 0.21;
Live 13; Mismatches 19
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Sequence 13089, Application US/09949016

; Sequence 13089, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
FILE REFERENCE: CLOOL307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-00-09
PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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US-09-328-352-1708
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1708
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APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT PELICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 1708

LENGTH: 2022
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 13089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
NAME/KEY: misc_feature
LOCATION: (1)...(89689)
OTHER INFORMATION: n =
                                                                                       TYPE: DNA
ORGANISM: Human
                                                                     FEATURE:
                                                                                                                                   ENGTH: 89689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         588 ATTAGGTTAACTATTTAGTTTTACTGTTCAGGATGCCCTATTGGCAGCCCCATAATATCCA 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 UGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUAGCUUUACUAAUCA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29,
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    A, T, C or
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    G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 6
US-09-949-016-15830
; Sequence 15830, Application US/09949016
    patent No. 6812339
    patent No. 6812339
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US-09-949-016-13539
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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, NAME/KEY: misc feature
; LOCATION: (1)...(314798)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13539
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 314798
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                 76 AGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAGAUACGUCACAGGAGA 135
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Similarity 43.1%;
53; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Mismatches
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Pred. No. 15;
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    ASSOCIATED OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 314798;
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          THEREOF
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US-09-949-016-144624
; Sequence 144624, Application US/09949016
; Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No. 6632636 40; PUBLICATION INFORMATION:
US-09-596-002-40
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; ORGANISM: Human
US-09-949-016-15830
                                                      RESULT 8
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SEQ ID NO 40
LENGTH: 119211
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Patent No. 6632636
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SEQ ID NO 15830
LENGTH: 192506
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Best Local Similarity
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Best Local S
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TITLE OF INVENTION: DOOS-4 US
FILE REPERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237.768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117374 TTTCAGCTTTGATACT 117389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117314 ATTTTCACAGATÁATTTGAGÁACTGAAAATGTTGTTTTTAAAACAACTCTCATTTAAAG 117373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE: CL001307
                                                                                                                                                                                           72121 CAAATTTTGGTGATATCTTAAGCTTTTGGCGATCCTGATGCTGACATCATTACCGAAAAAG
                                                                                                                                                     116 UCUAGAUACGUCACAGGAGAGCAUACGCUAGGUCGCGUUGACU 158
                                                                                                                                                                                                                                56 CAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AUCUUGCGCGAUAAAUGCUGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCU 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 АUUUĄGCUUUACUĄAU 87
                                                                                                                                                                                                                                                                      41; Conservative
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25; Conserv
                                                                                                                 ACAACCCAAAACACCAAAAAAGCAGATTGATCGTCGTTTTCACT 72019
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                                                                                                                                                                                                                                                                                        15.9%;
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32.9%; Pred. No. 20;
tive 21; Mismatches 30; Indels 0
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                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                        Score 27.8;
Pred. No. 20
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                      47; Indels
                                                                                                                                                                                                                                                                                                          Length 119211;
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144624
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                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecalis US-09-134-000C-1149
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APPLICANT: LYND DOUGETTE-Stamm et al
APPLICANT: LYND DOUGETTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-15
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 144624
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SEQ ID NO 1149
LENGTH: 1374
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                          Query Match
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                          / Match 15.8%; Score 27.6; Di
Local Similarity 36.6%; Pred. No. 3.1;
nes 30; Conservative 18; Mismatches
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588 TTTCAGCTTTGATA 601
                                                                                       394 ATTCCTGGGAGTGATGGCGTCATTGATTCTGTCGAAGAAGCGTTGACGATTGCTGAAGAA 453
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454 ATTGGTTÁCCCÁGTGÁTGTTAÁ 475
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                                        61 CUUGGUUAGCUAUUUAGCUUUA 82
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                                                                                                                                  1 AGUGUUGUGAUCUUGCGCGAUAAAUGCUGACGUGAAAAACGUUGCGUAUUGCUACAACA 60
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Pred. No. 2.1;
O; Mismatches 29;
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RESULT 10
US-09-270-767-4977
; Sequence 4977, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

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ORGANISM: Drosophila melanogaster US-09-270-767-4977
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US-09-270-767-20259
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US-08-956-171E-205/c
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4977
SEQ ID NO 4977
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APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT PELICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20259

LENGTH: 700

TYPE: DNA
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Best Local Similarity
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Matches
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Patent No. 6703491
                                                                                                                                  Sequence 205, Application US/08956171E Patent No. 6593114
GENERAL INFORMATION:
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APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
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Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27.4; DB Pred. No. 2.8; 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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SEQUENCE DESCRIPTION: SEQ ID US-08-956-171E-205
                                                                                                                                                                                                                                                 US-08-781-986A-205/c
; Sequence 205, Application US/08781986A
; Patent No. 6737248
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                                                                                                                                                                                                                                                                                                      RESULT 13
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REGISTRATION NUMBER: PB246
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 16397 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Charles
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                           APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staph
                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                    ZIP:
                                                                                                       CITY: Rockville
                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                     COUNTRY:
                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                               10332 AAATTTGTTGATGGTAAAAAGTTCGTATCGCTAAAAAATCTGGCGAAGAAATTAAMTCT 10273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                             10272 AATAATTAATA 10262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 AUAAAUGCUGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUU 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                    20850
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: double TOPOLOGY: linear
                                                                     Maryland
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                               ACUAAUCAAGA
                                                                                                                          9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9410 Key West Avenue
                                                                                                                                               Genome Sciences,
                                                                                                                                                                               Staphylococcus aureus Polynucleotides 5255
                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.7%; Score 27.4; I
42.3%; Pred. No. 11;
tive 14; Mismatches
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MSDOS version 6.2

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CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: US 60/194,648
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09824734
Patent No. 6727408
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.7%; Score 27.4; DB 3; Length 16397; Best Local Similarity 42.3%; Pred. No. 11; Matches 30; Conservative 14; Mismatches 27; Indels 0;
                 NAME/KEY: CDS
LOCATION: (459)..(550)
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: (631)..(708)
OTHER INFORMATION:
NAME/KEY: CDS
                                                                                                                                                            NAME/KEY: CDS
LOCATION: (1)..(226)
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: (330)..(380)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ZHU, JIAN-KANG
APPLICANT: SHI, HUAZHONG
APPLICANT: ISHITANI, MUADBU
APPLICANT: STEVENSON, BECKY
APPLICANT: STEVENSON, BECKY
APPLICANT: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-824-734-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 309-8510
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 16397 base pairs
TYPE: 16397 base pairs
                                                                                                                                                                                                                                                                                    LENGTH: 6076
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Benson, Bob
REGIZENCE JOCKET NUMBER: 98
REFERENCE JOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MSDOS version 6.:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 16397 base pairs
TYPE: nucleic acid
STRANDEDICE double
TORNOLOGY. 15000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10332 AAATTTGTTGATGGTAAAAAAGTTCGTATCGCTAAAAAATCTTGGCGAAGAAATTAAMTCT 10273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10272 AATAATTAATA 10262
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(804) .. (961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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NAME/KEY: CDS
; LOCATION: (5771)..(6073)
; OTHER INFORMATION:
US-09-824-734-1
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                                                                                                                           Query Match 15.5%; Score 27.2; DB 3; Best Local Similarity 36.1%; Pred. No. 8.8; Matches 26; Conservative 18; Mismatches 28.
                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (5375)..(5673)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (1432)..(1484)
OTHER INFORMATION:
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LOCATION: (1235)...
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: (1044)..(1145)
OTHER INFORMATION:
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LOCATION: (1738)..(1782)
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: CDS
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: CDS
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                              THER INFORMATION:
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OCATION: (5003)..(5273)
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OCATION: (3222)..(3453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AME/KEY: CDS
OCATION: (28)
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                                                                                                                                                                                                                                                                                                                                                                                OCATION: (4712)..(4915)
 1765
                                                               1705 GTGTGATATAAATTTTCCCGGTAACTTGTGCAGGGAAATGGTTGCATATATTTGCAAACAC 1764
                              62 UUGGUUAGCUAU 73
                                                                                              2 GUGUUGUGAUCUUGCGCGAUAAAUGCUGACGUGAAAACGUUGCGUAUUGCUACAACAC 61
TTTGATATTTAT 1776
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                                                                                                                               28;
                                                                                                                                                            Length 6076;
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                                                                                                                               Gaps
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RESULT 15 US-09-949-016-196049/c ; Sequence 196049, Application US/09949016

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTEN; J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR TILING DATE: 2000-19-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
SEQ ID NO 196049
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-196049
Search completed: December 22, 2005, 15:30:29 Job time : 75.5994 BECB
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                                                                                                                                                                                                  381 CTCAAAATCCCCCTCTAAAAAGCATATGCTA 351
                                                                                                                                                     115 GUCUAGAUACGUCACAGGAGAGCAUACGCUA 145
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
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                                                   0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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     222098777322209877654322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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7 US-10-088-750B-7
9 US-10-257-737-1
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9 US-10-450-763-7997
7 US-10-282-122A-8963
7 US-11-097-143-40165
7 US-10-088-750B-4
7 US-10-088-750B-4
8 US-10-741-600-11743
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9 US-10-765-790-89
9 US-10-367-094-93
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9 US-09-925-065A-306806
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               Sequence 7, Appli
Sequence 1, Appli
Sequence 69060, Ap
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Sequence 8963, Appli
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Sequence 17743, Appl
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Sequence 93, Appl
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Sequence 6827, Ap
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Sequence 6083, Ap
Sequence 5083, Ap
Sequence 3085, A
Sequence 305546, A
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Sequence 138, Ap
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| US-09-925-065A-306805 | US-09-925-065A-783500 | US-09-925-065A-799026 | US-09-423-093A-4 | US-10-425-115-13207 | US-10-021-323-17254 | US-10-021-323-8870 | US-10-088-750B-5 | US-10-027-632-115403 | US-10-027-632-115403 | US-10-437-963-39314 | US-10-027-632-156003 | US-10-027-632-156002 | US-10-027-632-156001 | US-10-027-632-156003 | US-10-027-632-156002 | US-10-027-632-156001 | US-09-925-065A-27086 | US-09-925-065A-27085 | US-09-925-065A-27083 | US-09-925-065A-27082 |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| 306805, | 783500, | 799026, | 4, Appli | 13207, A | 17254, A | 8870, Ap | 5, Appli | 115403, | 115403, | 39314, A | 156003, | 156002, | 156001, | 156003, | 156002, | 156001, | 27086, A | 27085, A | 27083, A | 27082, A |

ALIGNMENTS

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Sequence 7, Application US/10088750B

Publication No. US20040166486A1

GENERAL INFORMATION:
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: NAKASHIMA, Nobuhiko
TITLE OF INVENTION: A CULIVITY
FILE OF INVENTION: A CULIVITY
FILE OF INVENTION NUMBER: US/10/088,750B
CURRENT APPLICATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP 2001-016746
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/0641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 187
; TYPE: RNA
; ORGANISM: Rhopalosiphum Padi Virus
US-10-088-750B-7
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US-10-088-750B-7
                                                                                                                                                                                                                                              Query Match 100.0%; Score 175; DB 7; Best Local Similarity 100.0%; Pred. No. 7.3e-51; Matches 175; Conservative 0; Mismatches 0;
                        121 AUACGUCACAGGAGAGCAUACGCUAGGUCGCGUUGACUAUCCUUAUAUAUGACCU
                                                                                 61 CUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCACAAAAGUCUAG
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RESULT 2
US-10-257-737-1/c
US-10-257-737-1/c
; Sequence 1, Application US/10257737
; Publication No. US20050164354A1
; GENERAL INFORMATION:

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                                                                                     US-10-972-079-69060
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APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: KERR, Richard
APPLICANT: BATES, Stephen
APPLICANT: HOLM, Tom
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SEQ ID NO 1
      Matches
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CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIN version 3.1
SEQ ID NO 69960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69060, Application US/10972079 Publication No. US20050153317A1
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                                            Query Match
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APPLICANT: RENAULT, PIETE
APPLICANT: RENAULT, PIETE
ACTIC ACID BACTERIA MUTANTS OVERPRODUCING EXOPOLYSACCHARIDES
FILE REFERENCE: 3339/249437
CURRENT APPLICATION NUMBER: US/10/257,737
CURRENT FILING DATE: 2002-10-16
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER TITLE OF INVENTION: LIVESTOCK FILE REFERENCE: MMI1110-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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LOCATION: (2169)..(3092)
                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(16)
OTHER INFORMATION: n is any nucleotide
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                                                                                                                                                                        FEATURE:
                                                                                                                                                                                  TYPE: DNA
ORGANISM: Chicken 19866894340881_1
                                                                                                                                                                                                                                 ENGTH: 599
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nes 48; Conservative
Match 17.9%; Score 31.4; Di
Local Similarity 35.5%; Pred. No. 2.8;
es 43; Conservative 22; Mismatches
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BESANCON-YOSHPE, Iris
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40.7%; Pred. No. 5.9;
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FEATURE:
| NAME/KEY: SIMILAR | LOCATION: (114).. (965) | OTHER INFORMATION: 38% homologous to Dictyostelium discoideum TipD, accession | OTHER INFORMATION: number AF019236, Smith-Waterman Score=497. US-10-450-763-7997
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US-10-450-763-7997/c
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Publication No. US20050196754A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10088750B Publication No. US20040166486Al GENERAL INFORMATION:
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LENGTH: 2398
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Best Local
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CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANAMORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting Translation
TITLE OF INVENTION: Activity
FILE REFERENCE: 3190-015
CURRENT FILINGIATION NUMBER: US/10/088,750B
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
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ORGANISM: Homo sapiens
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подпрости подпрости подпрости подпрости подпро
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US-10-282-122A-8963
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PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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SEQ ID NO 3
LENGTH: 201
TYPE: RNA
ORGANISM: Drosophila C Virus
                                                                                 SOFTWARE: Pat
SEQ ID NO 8963
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APPLICANT:
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Carlos
Carlos
Cheryl
Rot
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: PCT/JP01/00641
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 12
                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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              TYPE: DNA ORGANISM: Acinetobacter
                                                                 LENGTH: 1992
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Local Similarity 66.2%;
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                                                                                                             PatentIn version 3.1
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck,
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Pred. No. 2.1;
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APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

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                                                                                                                                                                                      RESULT 8
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                                                                                      Sequence 4, Application US/10088750B Publication No. US20040166486A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 38
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Publication No. US20050208558A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: NAKASHIMA, Nobuhiko
APPLICANT: KANANORI, Yasushi
TITLE OF INVENTION: A Novel Higher-Order Structure With Promoting
TITLE OF INVENTION: Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/191,637 PRIOR FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 22188
TYPE: DNA
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                19567 CGTAAATGAACCATAATTGGATCGCTATATAGATTTTTTTATTCGATGGTGATGCCTCAGG
                                                                                                                                                                                                                                                         19507
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                                                                                                                                                                                                                                                                                                                                                                                           46 CGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAG
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38; Conserv
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                                                                                                                                                                                                                                                         CTTAGATCTGTTTTCGTAAGTGGAAGCAGAGCATACGCGAG 19467
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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44.7%; Pred. No. 8.6;
tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
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                            Translation
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(S-10-737-082-89)
(Sequence 89, Application US/10737082
(Publication No. US20050130170A1
(GENERAL INFORMATION:
APPLICANT: Bayer Healthcare LLC
(APPLICANT: Beard, Chris
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Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES TITLE REFERENCE: CLO01499
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 17743
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CURRENT APPLICATION NUMBER: US/10/088,7508
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: JP P2001-016746
PRIOR FILING DATE: 2001-01-25
PRIOR FILIAGION NUMBER: PCT/JF01/00641
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
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SOFTWARE: PatentIn version 3.2
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TYPE: RNA
ORGANISM: Cricket Paralysis Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE: misc feature NAME/KEY: misc feature LOCATION: (1)...(61718)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
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TYPE: DNA
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Gannon, Allison
               Burgess,
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Pred. No. 4.8;
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-765-790-89
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US-10-765-790-89
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US-10-367-094-93
; Sequence 93, Application US/10367094
; Publication No. US20040170982A1
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Publication No.
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Best Local Similarity
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PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
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TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
CURRENT APPLICATION UNMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
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CURRENT APPLICATION NUMBER: US/10/737,082
CURRENT FILING DATE: 2003-12-16
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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Li, Zheng
IITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 29.4; DB 9;
; Pred. No. 1.2e+02;
16; Mismatches 51;
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE; ELITA, 011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT ETLING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR PRICHED FROM NUMBER: 60/206,848 PRIOR PRICHATION NUMBER: 60/206,848 PRIOR PRICHATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/207,727
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; ORGANISM: Homo sapiens
US-10-367-094-93
                                                                                                                                      Query Match
Best Local &
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CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 149062
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APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001500
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3908
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecalis -09-815-242-3908
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-23
                                                                                                                                      Local Similarity
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Yamamoto, Robert T.
Xu, H. Howard
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39.6%; Pred. No. 1.3e+02;
vative 16; Mismatches 51;
                                                                                                                            16.7%; Score 29.2;
36.6%; Pred. No. 23;
                                                                                 19; Mismatches
                                                                                                                                                                       DB 3;
                                                                            33;
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                                                                                                                                                                       Length 1329;
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GENERAL

INFORMATION:

APPLICANT: Roemer,

APPLICANT:
APPLICANT:

Jiang, Boone,

Terry Bo Charles

Bussey,

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RESULT 15
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-23
PRIOR PRILING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
Sequence 6083, Application US/10741849 Publication No. US20050019931A1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1371)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-12-22
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                                                                                                                      451 ATTGGTTACCCAGTTATGTTAA
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o. US20020061569A1
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                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu, H. Howard
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                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                      16.7%; Score 29.2; 1
36.6%; Pred. No. 23;
tive 19; Mismatches
                                                                                                                         472
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                                                                                                                                                                                                                                                                                                                               Length 1371;
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TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of TITLE OF INVENTION: Use
FILE REFERENCE: 10182-023-999
CURRENT APPLICATION UNMERR: US/10/741,849
CURRENT APPLICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2002-12-19
PRIOR PAPELICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2002-12-19
NUMBER: OF SEQ ID NOS: 8000
SOSTWARE: PatentIn version 3.2
SEQ ID NO 6083
LENGTH: 1905
TYPE: NON
ORGANISM: Candida albicans
US-10-741-849-6083
Query Match
Best Local Similarity 31.2%; Pred. No. 31;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatches 40; Indels 0; Gaps 0;
Matches 29; Conservative 24; Mismatche
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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      9
                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Match
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  15.8 1964
15.5 107
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15.0 103931
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14.9 1071
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175
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Copyright (c) 1993 - 2005 Compugen Ltd.
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               US-10-995-561-13326
US-10-750-185-28773
US-10-750-185-29226
US-10-750-185-29226
US-10-750-185-49272
US-11-17-187-193
US-10-793-626-1047
US-10-793-626-4242
US-10-793-626-4242
US-10-793-626-43130
US-10-793-626-43131
US-10-995-561-13254
US-10-995-561-13254
US-10-195-561-13254
US-10-750-185-61599
US-10-750-185-615991
US-10-750-185-58921
US-10-995-626-1333
US-10-995-626-1333
US-10-995-636-1333
US-10-995-636-1333
US-10-995-636-1333
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Sequence 13326, A
Sequence 28773, A
Sequence 61874, A
Sequence 49272, A
Sequence 1937, Ap
Sequence 1047, Ap
Sequence 3307, Ap
Sequence 3736, Ap
Sequence 4242, Ap
Sequence 4013, Ap
Sequence 4013, Ap
Sequence 54508, A
Sequence 54508, A
Sequence 54508, A
Sequence 28765, A
Sequence 29162, A
Sequence 29162, A
Sequence 58921, A
Sequence 13421, A
Sequence 13421, A
Sequence 13421, A
Sequence 13421, A
Sequence 4002, A
Sequence 4002, A
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| 24.2 | 24.2 | | 24.2 | | | 24.4 | 24.4 | 24.4 | 24.4 | | 24.4 | | | | | | | | | | |
| 13. | 13. | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13 | 13. | | | | | 14. | | | 14. | |
| 8 3671 | .8 2609 | .8 1969 | .8 1619 | _ | | 1.9 180654 | _ | .9 3092 | Ī | | _ | 9 1332 | 1 171423 | 1 51749 | 1 2864 | 1 1831 | 1 1534 | 1 201 | 2 164527 | 2 160213 | |
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| US-10-131-826A-141 | US-10-750-185-54446 | US-10-750-185-46387 | US-10-750-185-34664 | US-10-750-185-59183 | US-11-108-172-742 | US-11-121-086-58 | US-10-793-626-4180 | US-10-793-626-3714 | US-11-097-728-3 | US-10-750-185-41658 | US-10-750-185-58979 | US-10-793-626-1859 | US-11-121-086-85 | US-10-995-561-13245 | US-10-955-054A-165 | US-10-750-185-34142 | US-10-750-185-38375 | US-10-995-561-28817 | US-11-121-086-71 | US-11-121-086-103 | |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Sequence | Sequence | Sequence | Sequence | |
| 141, App | 54446, A | 46387, A | 34664, A | 59183, A | 742, App | 58, Appl | 4180, Ap | 3714, Ap | 3, Appli | 41658, A | 58979, A | 1859, Ap | 85, Appl | 13245, A | 165, App | 34142, A | 38375, A | 28817, A | 71, Appl | 103, App | |

ALIGNMENTS

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Sequence 13326, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
ITILE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRStSEQ for Windows Version 4.0
SEQ ID NO 13326
LENGTH: 61718
TYPE: DNA
ORGANISM: Homo sapiens
      RESULT 2
US-10-750-185-28773
US-10-750-185-28773; Application US/10750185; Sequence 28773, Application US/10750185; Publication No. US20050260803A1; GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MI GENOMICS, SUE K.
APPLICANT: KERR, Richard; APPLICANT: ROSENFELD, David
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US-10-995-561-13326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.3%; Score 30.2; DB 6; Length 6: Best Local Similarity 34.7%; Pred. No. 1; Matches 51; Conservative 23; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22966 GCAGCAGTTAACGCTGCAGTTCCCTGT 22992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22846 CGGGAGATGGGAGAGTGAAAAACCATGTCATTTACAATTTGATTAAAAAGCTTTTTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 ACGCUAGGUCGCGUUGACUAUCCUUAU 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCCTTTCACGTTTAAGCCTTTGCCGTTTTAAAAATTTCCCTTTCGTCACAGGGGATCAA 22965
DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
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FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOPTWARE: PATENTIN Version 3.1
SEQ ID NO 28773
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RESULT 4

US-10-750-185-29226

; Sequence 29226, Application US/10750185

; Publication No. US20050260603A1
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SEQ ID NO 61874
LENGTH: 1787
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
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ORGANISM: Bovine
-10-750-185-61874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, SUE K.
APPLICANT: KERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HOLM, TOM
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR EILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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TYPE: DNA
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PPLICANT: FANTIN, Dennis
ITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                              Local Similarity nes 40; Conserv
                                                                                                                               1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885 AGACATTGTCTGTAATCCTCAAAACCACCTTGAAAGGTAGACATAATTGTTTCTATTTC 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCCACAAAAGUCUAGAUACGUC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGATGAGGAACTGAGTGTTCGGGTTAAGTAACTTTA 982
                                                                                                                             GCAGAAACTGGACGGGTGAGATGTGGCCAGGCCATGAGGCTTGGTGACTTTCCTGAT 1072
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                                                                                                                                                                                                               UUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGUCGUGCAGCCCA 109
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          19866880589931
                                                                                                                                                                                                                                                                                              15.7%; Score 27.4; Di 34.2%; Pred. No. 2.3; tive 21; Mismatches
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US-10-750-185-29226
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; ORGANISM: Bovine 19866880857844
US-10-750-185-49272
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US-10-750-185-49272/c
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APPLICANT: MMI GENOMICS, I
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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APPLICANT: MMI GENOMICS,
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Best Local :
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Best Local Similarity
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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 854 TCTAAGTTATACAGTCTAGCTAATAAAAAGGCCAT 820
                                                                     914 GTTTTGTGAATTACTTAGAGATCTACCCAAATATATACGAACCAAATAACATCAAAACTT
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1 Similarity 33.8%; Pred. No. 1.9;
27; Conservative 20; Mismatches
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                                  64 GGUUAGCUAUUUAGCUUUACUAAUCAAGACGCCGU 98
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KERR, Richai
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                                                                                                                                              15.0%; Score 26.2; Di
36.8%; Pred. No. 5.9;
ative 17; Mismatches
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RESULT 6
US-11-117-187-193/c
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-193
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERWIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER: OF SEQ ID NOS: 4472

SOFTWARE: PSECHIIN Ver. 2.1

SEQ ID NO 1047

LENGTH: 1071
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
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TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: nucleic ac:
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              94 GCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
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                                                                                                                GAGAATTCGACAAGTTTTGGCTTAACAATTTTTTAGCAATACGATCTGCTTCATCATTAC 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description of Artificial Sequence: synthetic nucleic acid sequence
                                                                                                                                                                                                                                                                                          14.9%; Score 26; DB 6; Length 1071; 37.8%; Pred. No. 6.1; ative 16; Mismatches 40; Indels
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic;
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3736
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SEQ ID NO 2307
LENGTH: 1467
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SEQ ID NO 3736
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Best Local Similarity
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CURRENT FILLING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
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CURRENT FILING DATE: 2004-03-04
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2352
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2257
                                                                             2317 AAGCTGGCGTAGATGCATTAATTÁTTGATACAGCTCATGGTCATTCTAAAGGCGTTATTA 2258
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                                    86 AUCAAG 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
27; Conserv
ATCAAG 2252
                                                                                                                    AUGCUGACGUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 26; ilarity 40.9%; Pred. No. Conservative 14; Mismatc
                                                                                                                                                             Conservative
                                                                                                                                                                              14.9%; Score 26; DB 6; 40.9%; Pred. No. 8.7;
                                                                                                                                                             14; Mismatches
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                                                                                                                                                                                                 Length 2352;
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RESULT 11
US-10-793-626-3390/c
US-10-793-626-3390, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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Sequence 4242, Application US/10793626; Publication No. US20050255478A1
RESULT 12
\US-10-793-626-4013
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PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 4242
LENGTH: 2980
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3390
LENGTH: 3502
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APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                                                                 1155
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                                                                                                                          94
                                                                                                                                                                                                         34 GUGAAAACGUUGCGUAUUGCUACAACACUUGGUUAGCUAUUUAGCUUUACUAAUCAAGAC 93
                                                                                                                                                                                                                                                 34;
                                                                                 CAAGTCGTCGTCAACAATTGTTTAATTA 1126
                                                                                                                          GCCGUCGUGCAGCCCACAAAAGUCUAGAUA 123
                                                                                                                                                                GAGAATTCGACAAGTTTTGGCTTAACAATTTTTTAGCAATACGATCTGCTTCATCATTAC 1156
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                     14.9%;
                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                       Score 26; DB 6;
Pred. No. 10;
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: nucleic acid sequence US-10-793-626-4013
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US-10-995-561-13254/c
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publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13254, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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LENGTH: 3840
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
EILE REFERENCE: CLOO1559
CURRENT EPPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                     LENGTH: 65931
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                        Match 14.7%; Score 25.8; I
Local Similarity 31.9%; Pred. No. 47;
Les 43; Conservative 24; Mismatches
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                                                                                                                                                   62650
                                                                        62590 AAGTGTGAAGTTTTATAGTTTTCTAATAATTATTCAGTATTATCCCYTTCAGAGATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 AUCAAG 91
                                                                                                          ch 14.9%;
l Similarity 40.9%;
27; Conservative 1
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 GTAGGATÁCCACAGA 62516
                                     AUACGUCACAGGAGA 135
                                                                                                                                                 14;
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Pred. No. 11;
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                                                                                                                                                                                                                                                                  Length 65931;
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RESULT 14 US-10-750-185-61359/c

Sequence 61359, Application US/10750185 Publication No. US20050260603A1

INFORMATION:

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APPLICANT: ROSENFELD, DAVID
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
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PRIOR APPLICATION NUMBER
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
INUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 61359
US-10-750-185-61359
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; Sequence 54508, Application US/10750185
; Publication No. US20050260603A1
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                                                                                                                                                                                                                                                                                                                      Query Match 14.5%; Score 25.4; DB 6; Length 788; Best Local Similarity 37.3%; Pred. No. 8.9; Matches 31; Conservative 16; Mismatches 36; Indels
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                          362 ATAGATGTTGTTAAATTGCTAAGTTGTGTTCCAACCCTTTGTGATCTTATAGACTGT 303
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                                                                                                                                                                                                   22 AUAAAUGCUGAAGGUGAAAACGUUGCGUAUUGCUAACACACCUUGGUUAGCUAUUUUAGCUUU 81
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82 ACUAAUCAAGACGCCGUCGUGCA 104
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Search completed: December 22, 2005, 16:41:20 Job time : 167.698 secs

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